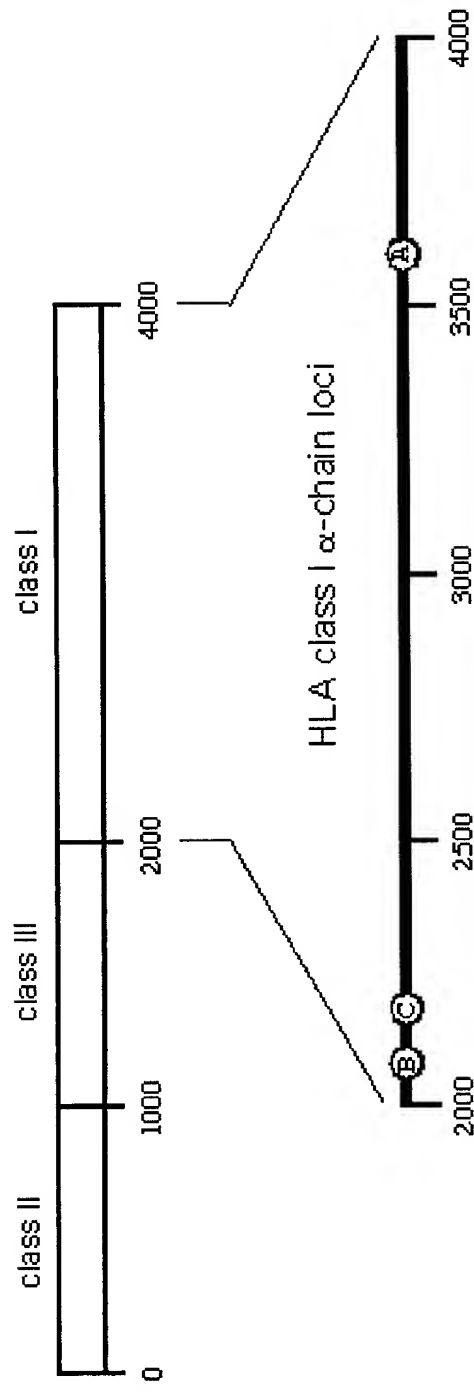


A



B

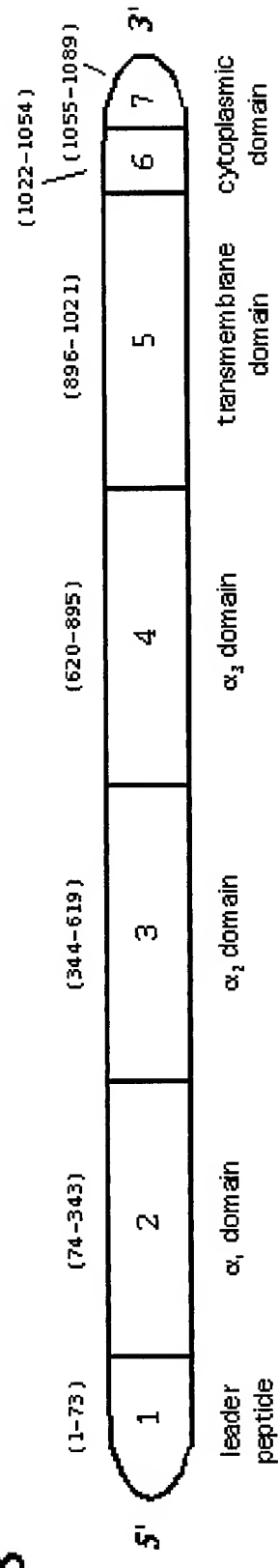


FIG. 1

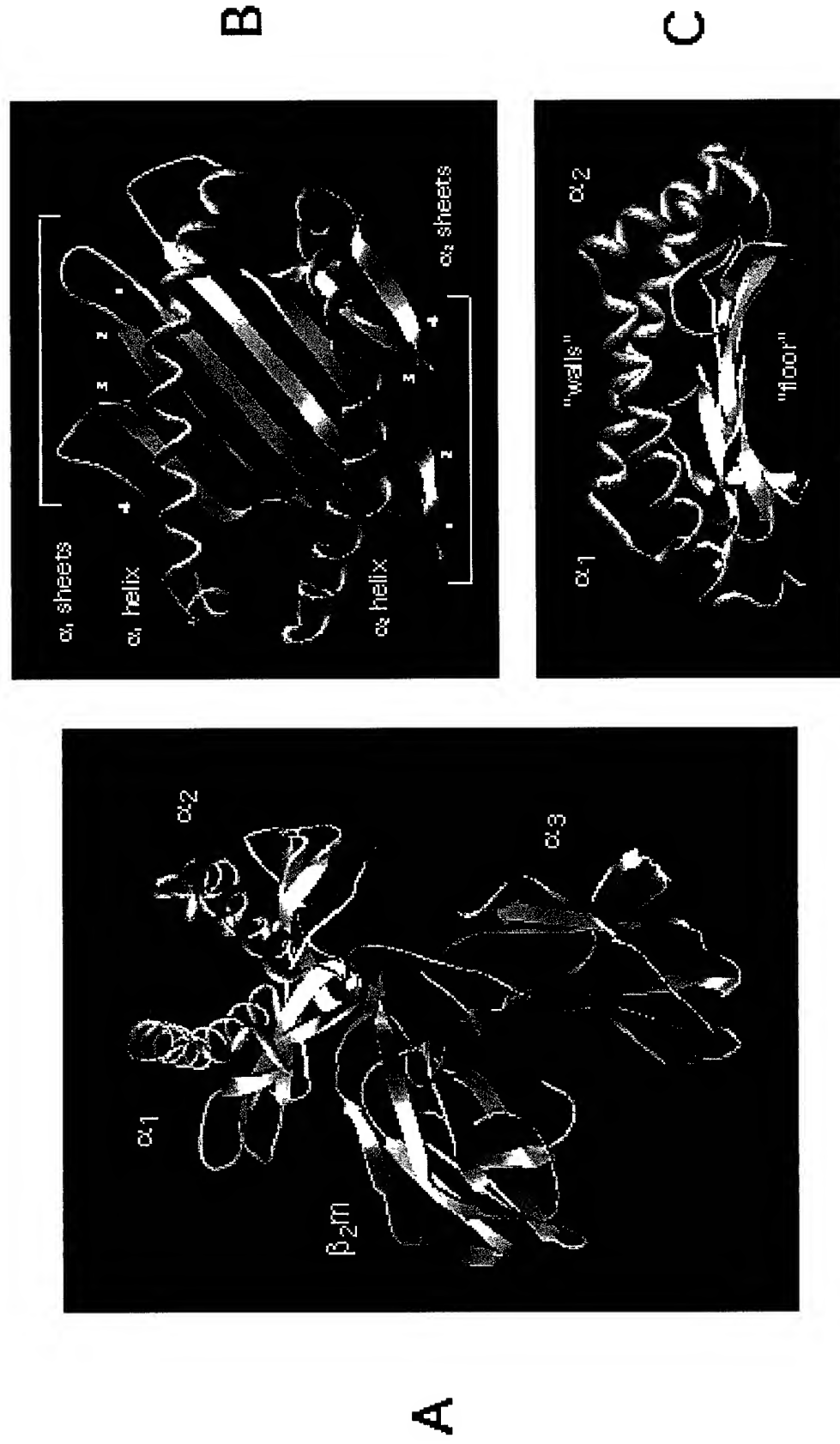


FIG. 2

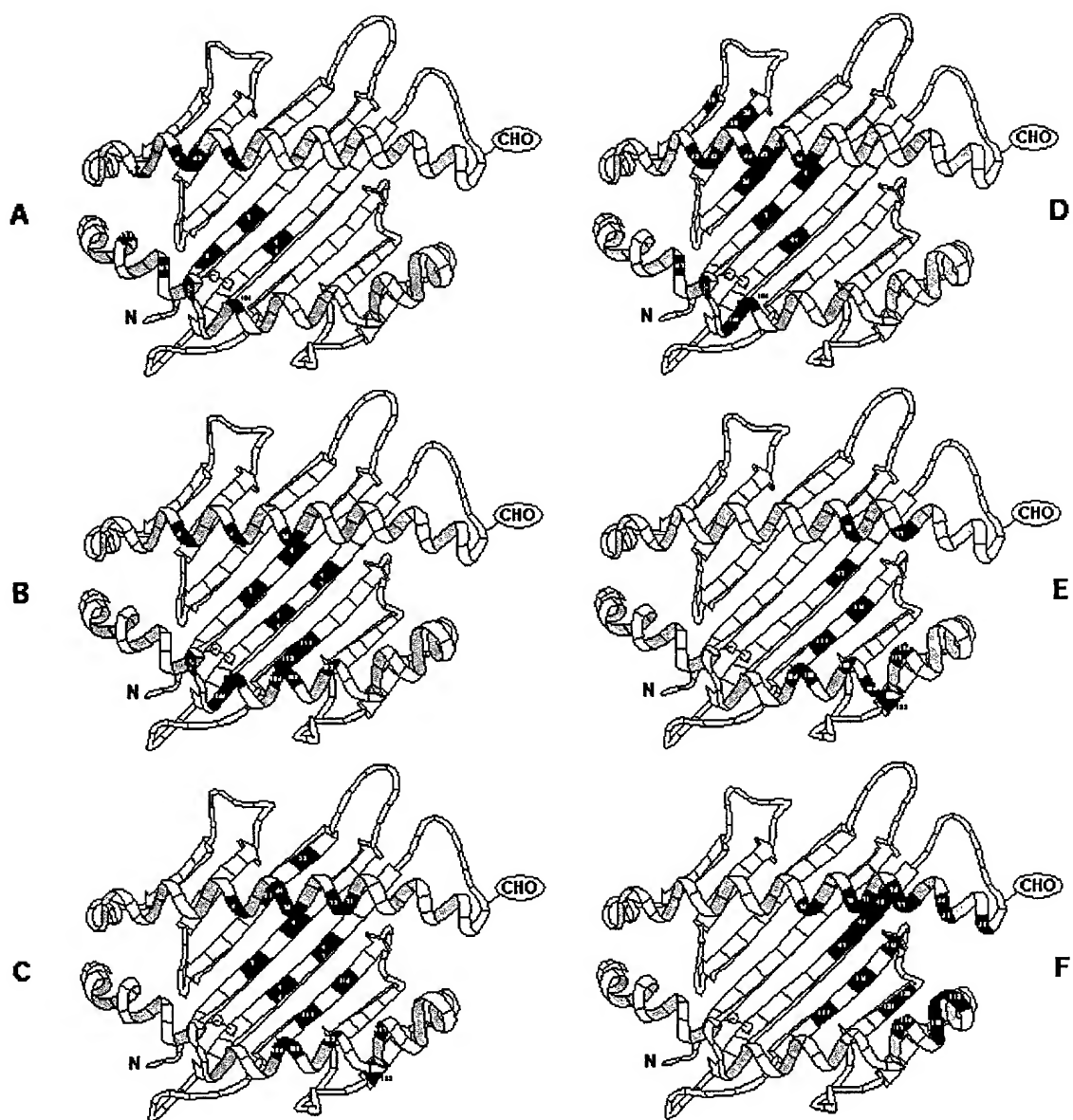


FIG. 3

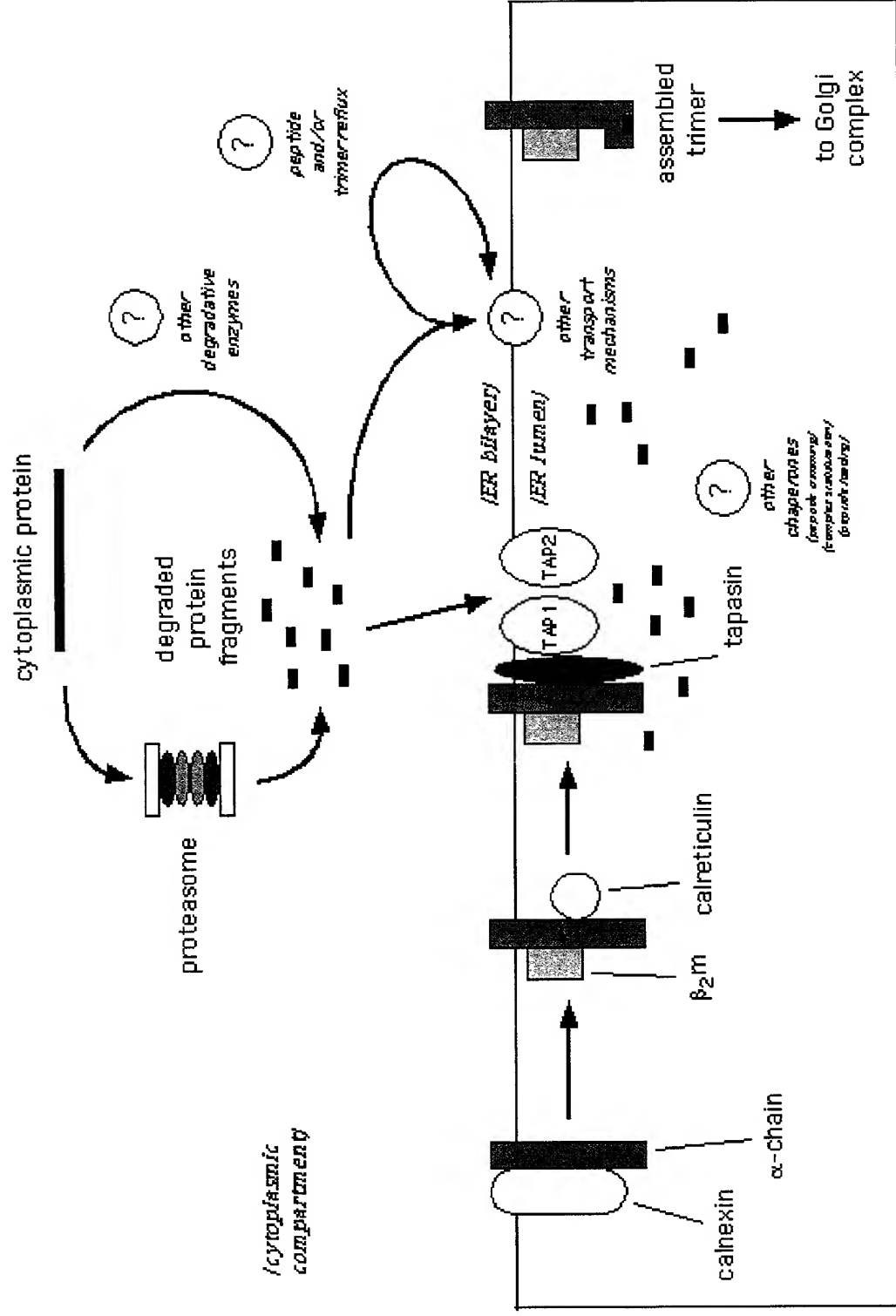


FIG. 4

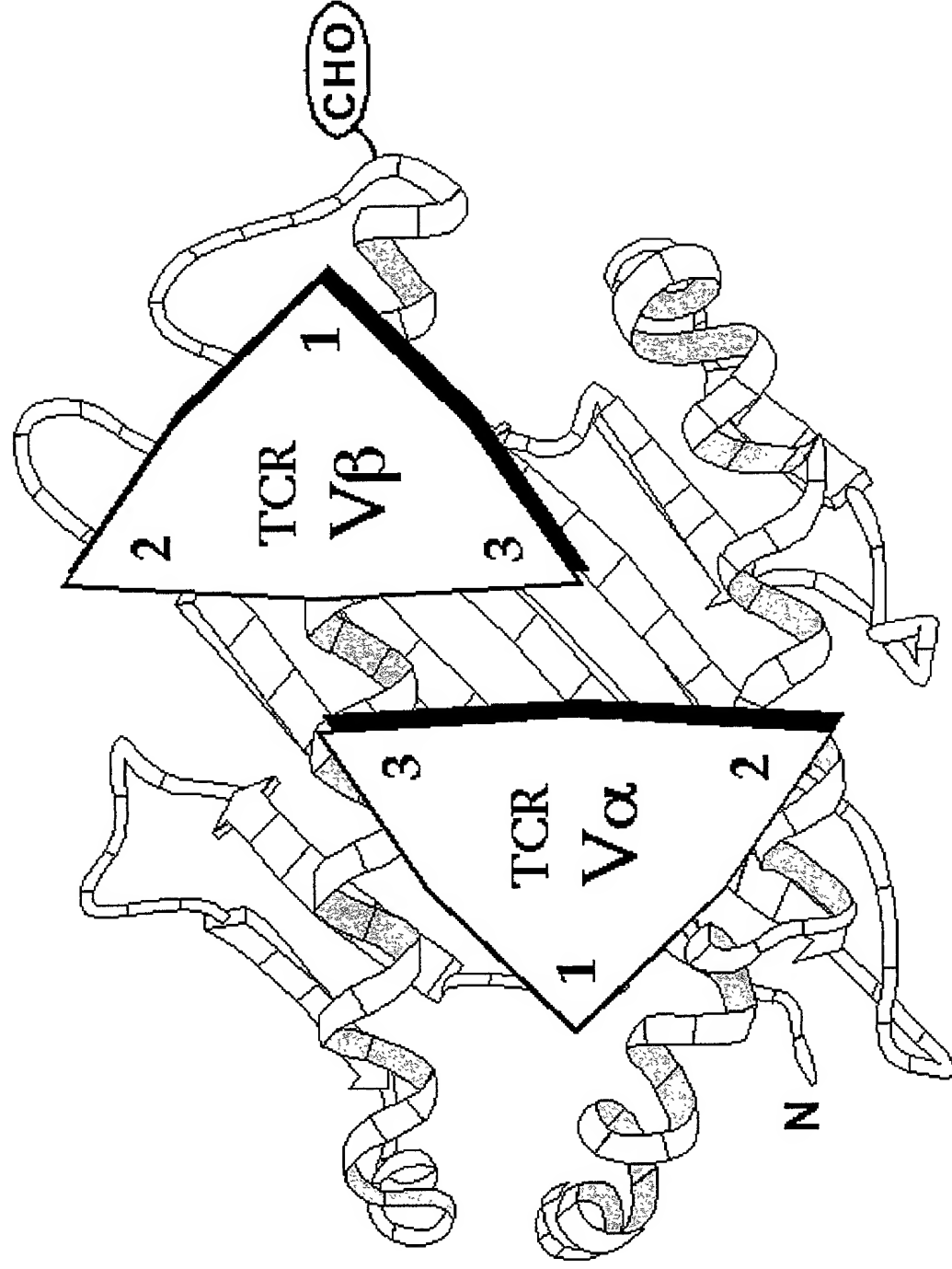


FIG. 5

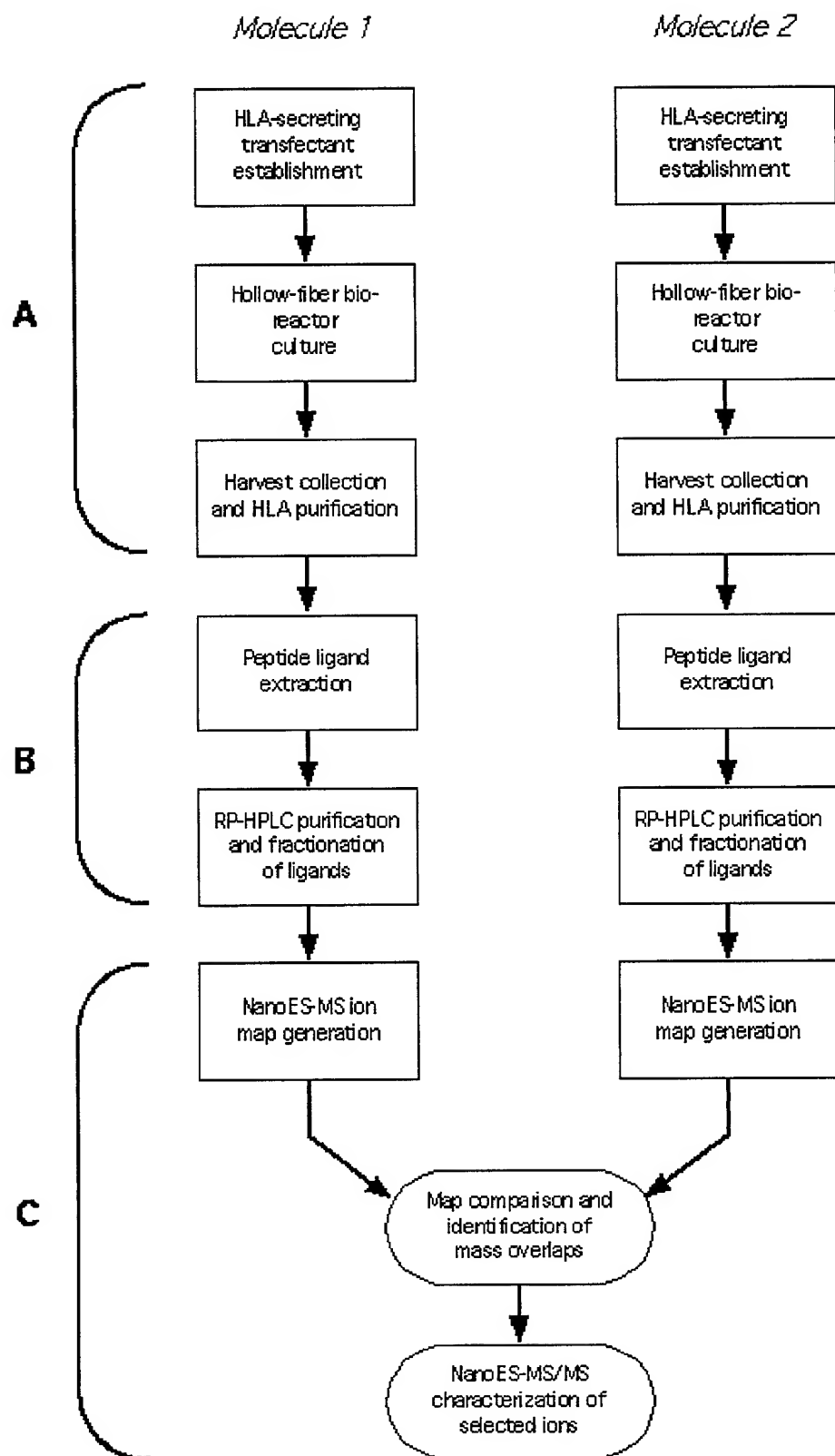


FIG. 6

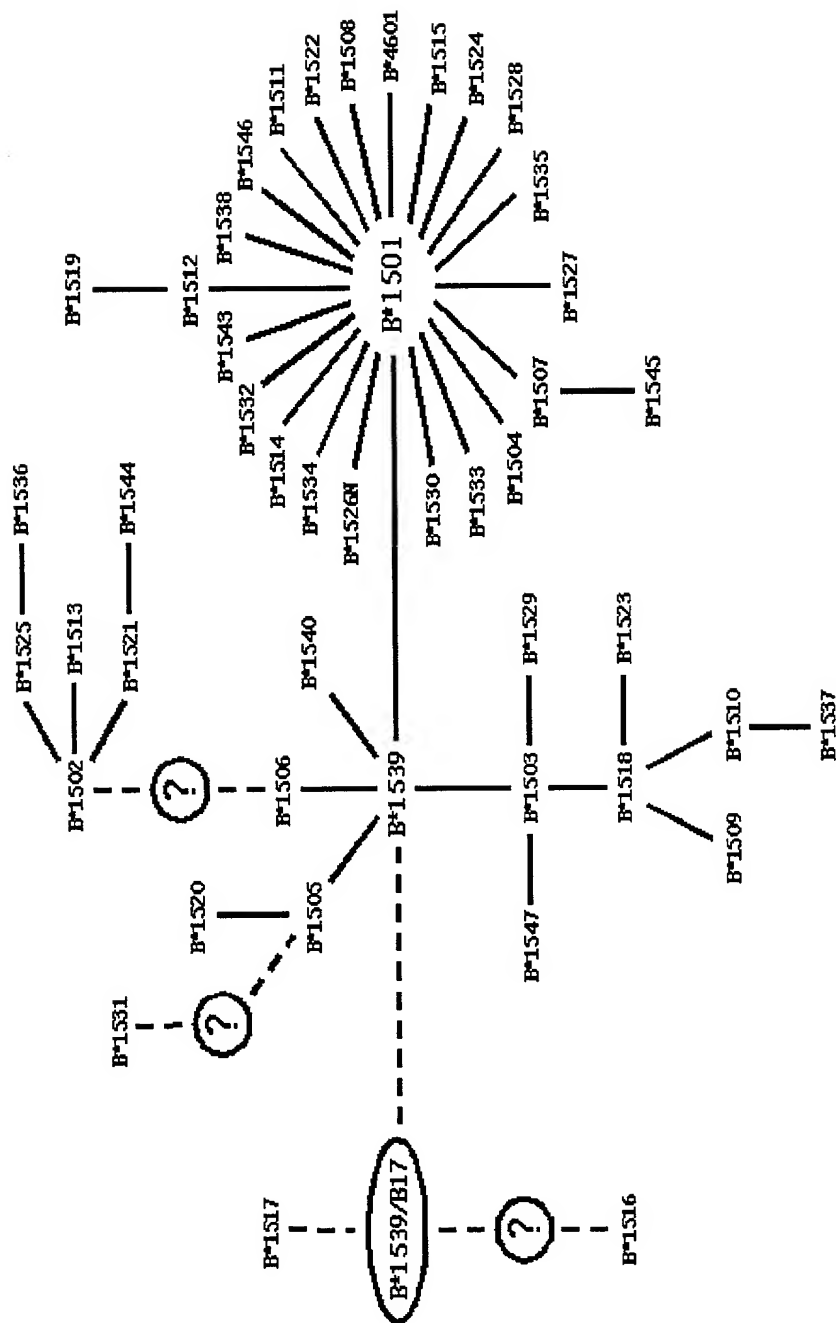


FIG. 7

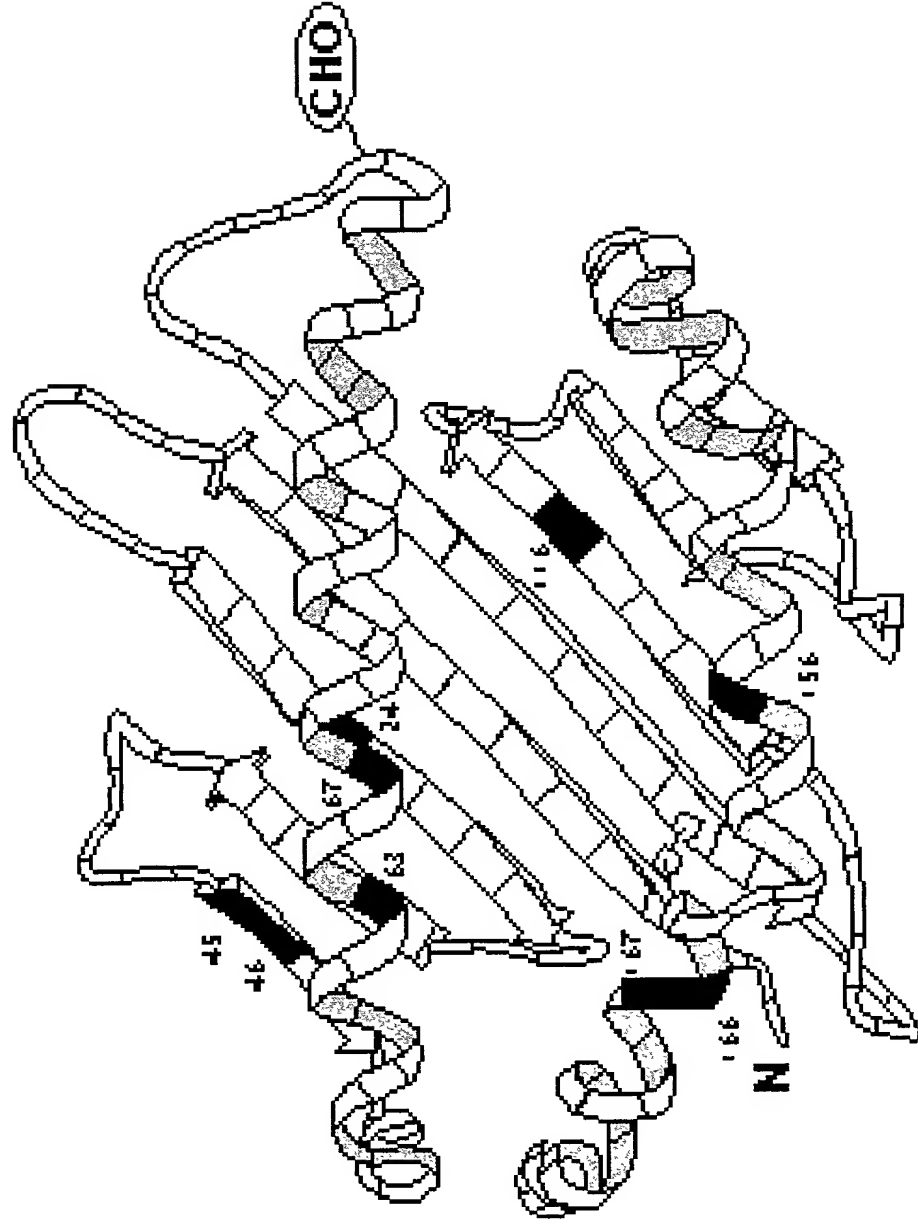


FIG. 8

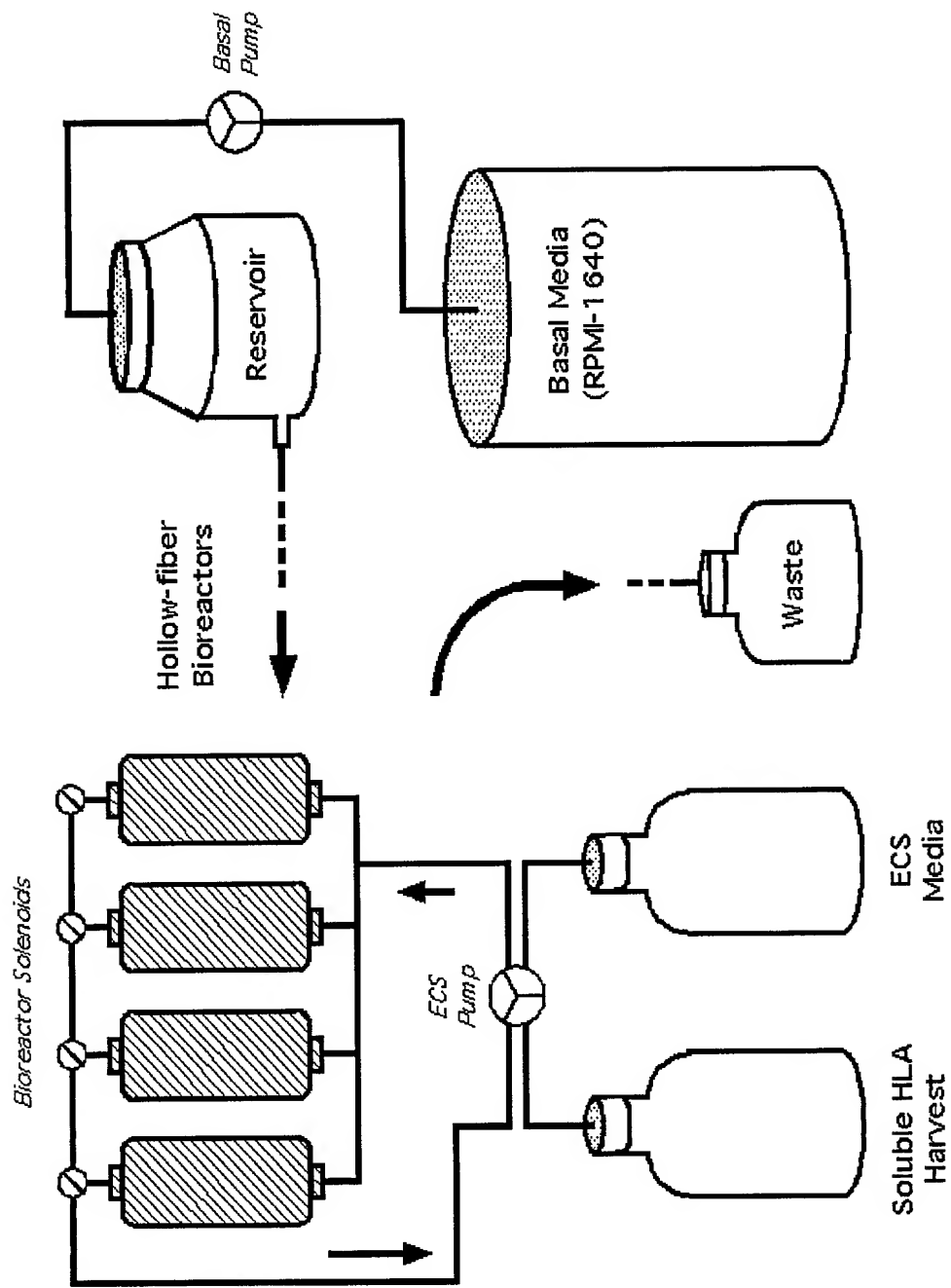


FIG. 9

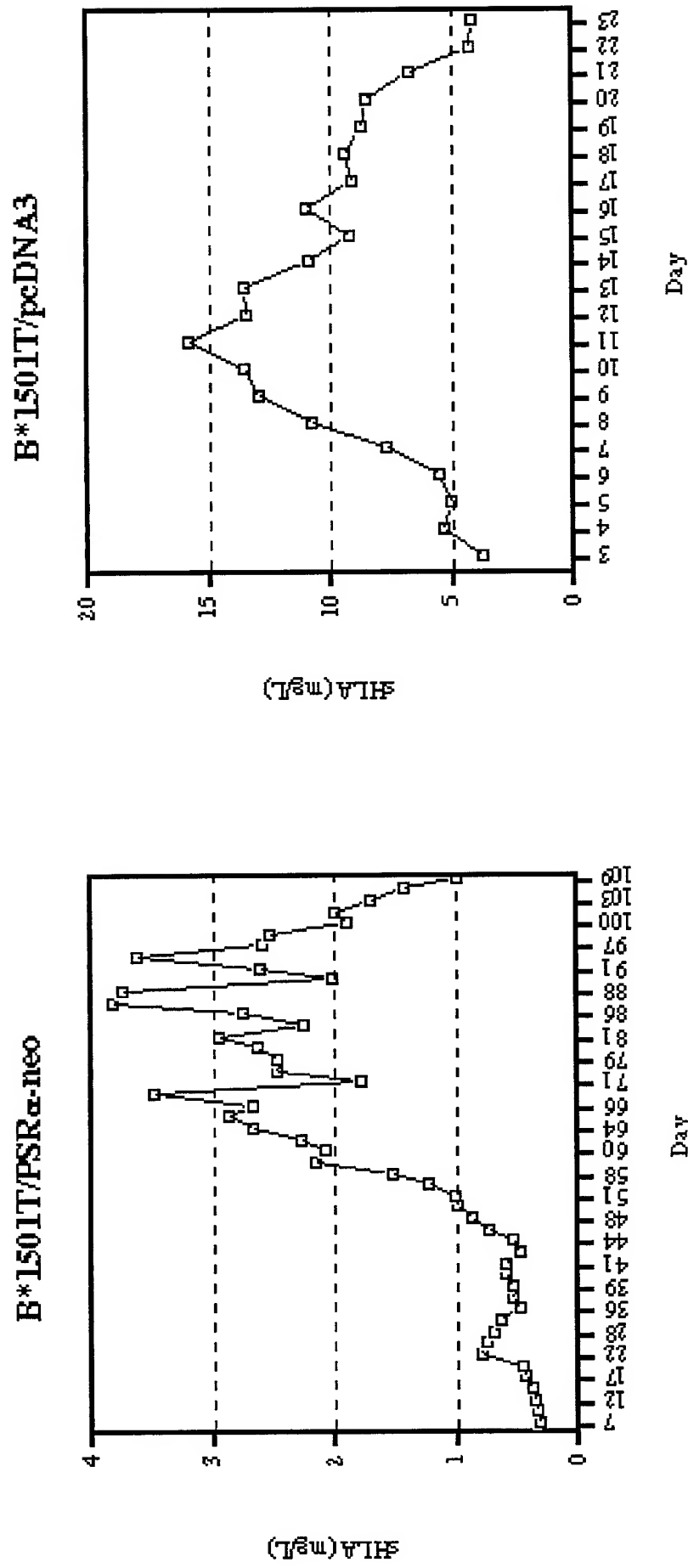


FIG. 10

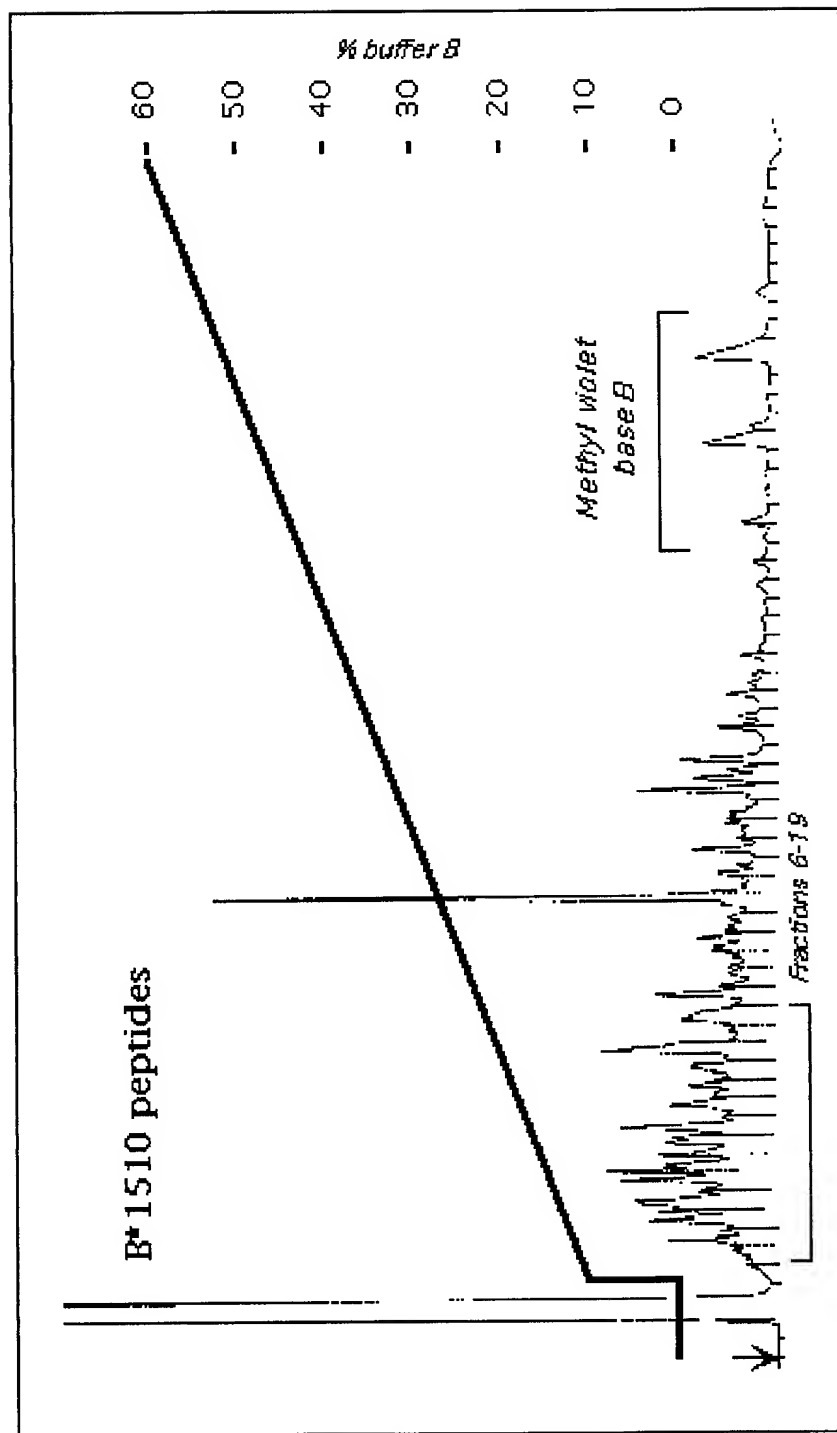
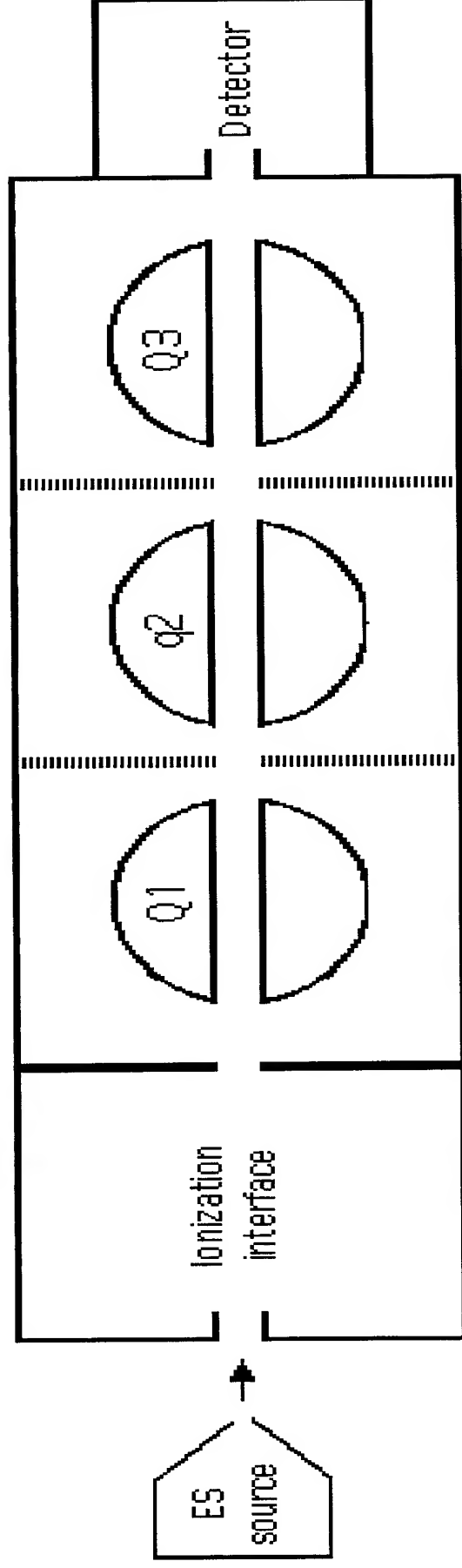


FIG. 11



Ion selection / transmission / collision

FIG. 12

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted April 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

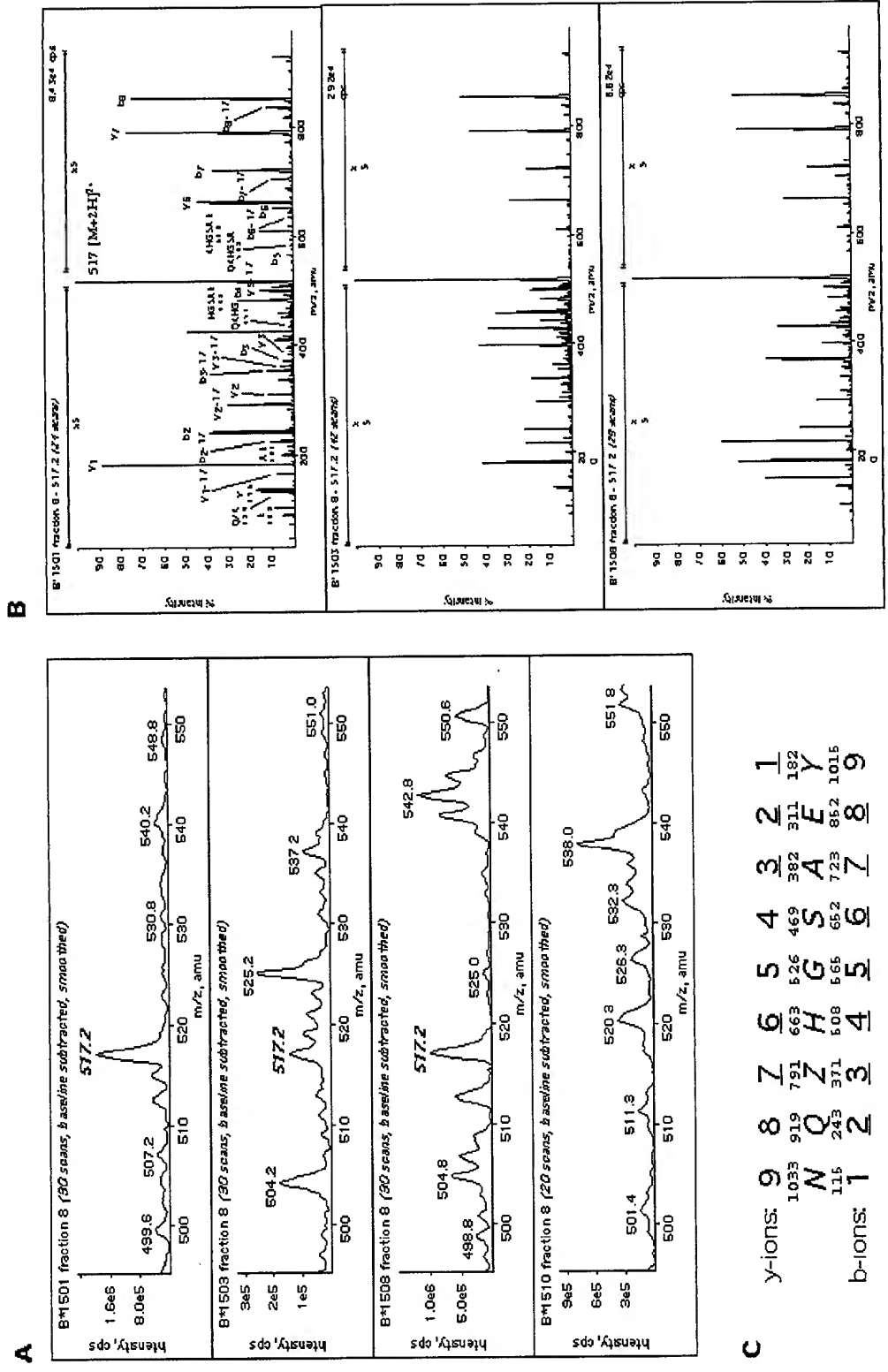
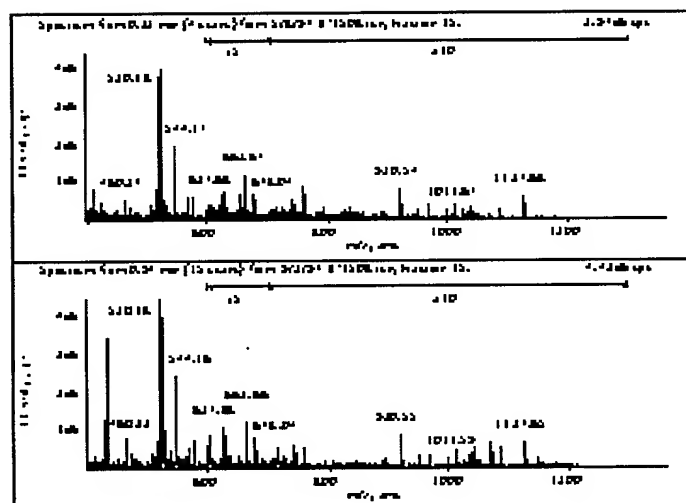
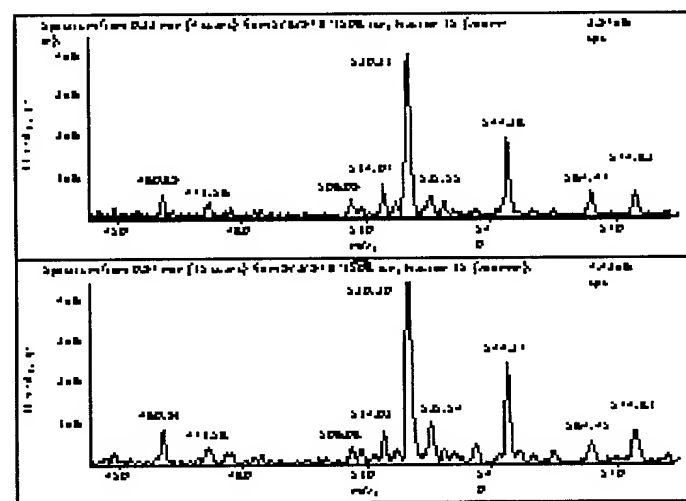


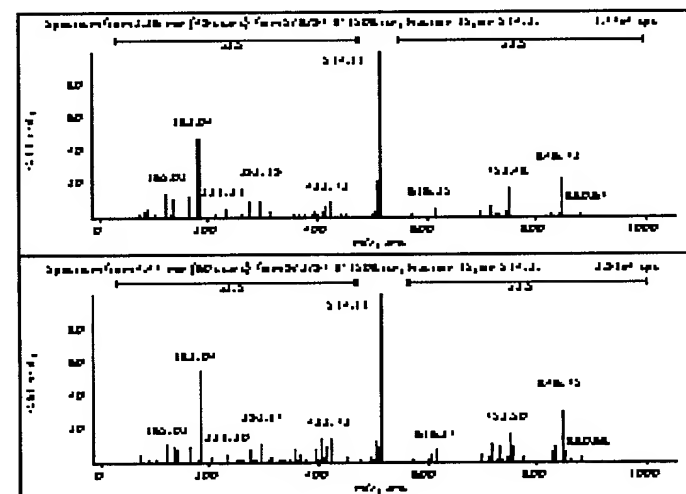
FIG. 13



A



B



C

FIG. 14

A (W6/32-purified B*1501 complexes)

position:	1	2	3	4	5	6	7	8	9	10	11	12	13	14
<i>dominant</i>	—	Q _(8.0)	K _(8.0)	—	—	—	—	—	Y _(4.0)	—	—	—	—	—
			F _(5.0)											
			R _(4.0)											
<i>strong</i>	—	M _(3.0)	Y _(3.0)	P _(2.5)	G _(2.0)	—	—	—	F _(3.0)	—	—	—	—	—
		L _(2.0)	P _(2.0)	D _(2.5)										
		V _(2.0)	N _(2.0)	G _(2.0)										
			H _(2.0)	E _(2.0)										

FIG. 15

B (BBM.1-purified B*1501 complexes)

position:	1	2	3	4	5	6	7	8	9	10	11	12	13	14
<i>dominant</i>	—	Q _(7.5)	—	—	—	—	—	—	Y _(4.0)	—	—	—	—	—
<i>strong</i>	—	P _(3.5)	F _(2.5)	P _(2.2)	I _(2.0)	—	—	—	F _(3.0)	—	—	—	—	—
		L _(2.5)	K _(2.5)	D _(2.0)										
		V _(2.0)	R _(2.0)	G _(2.0)										
			P _(2.0)											
			N _(2.0)											

FIG. 15 CONT'D.

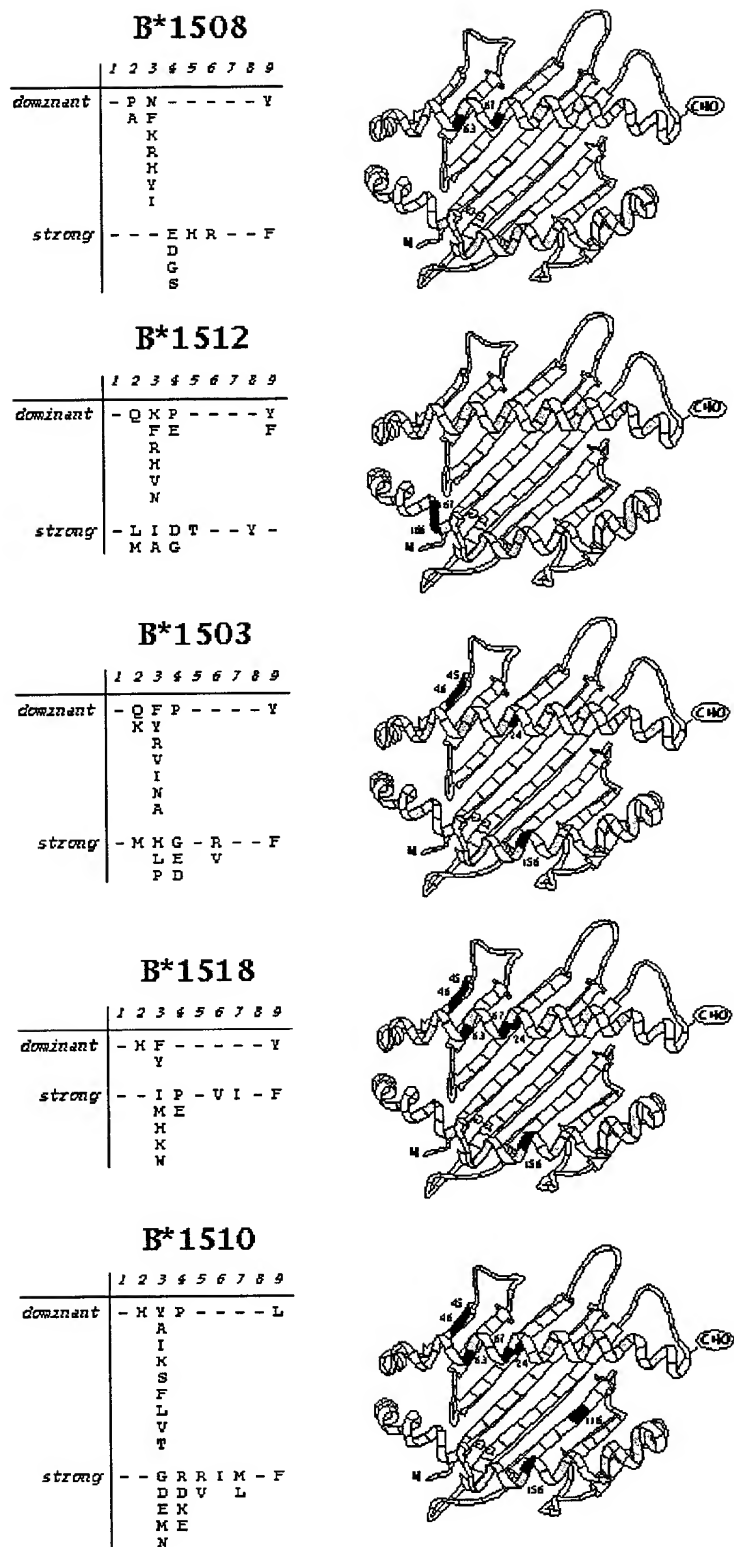


FIG. 16

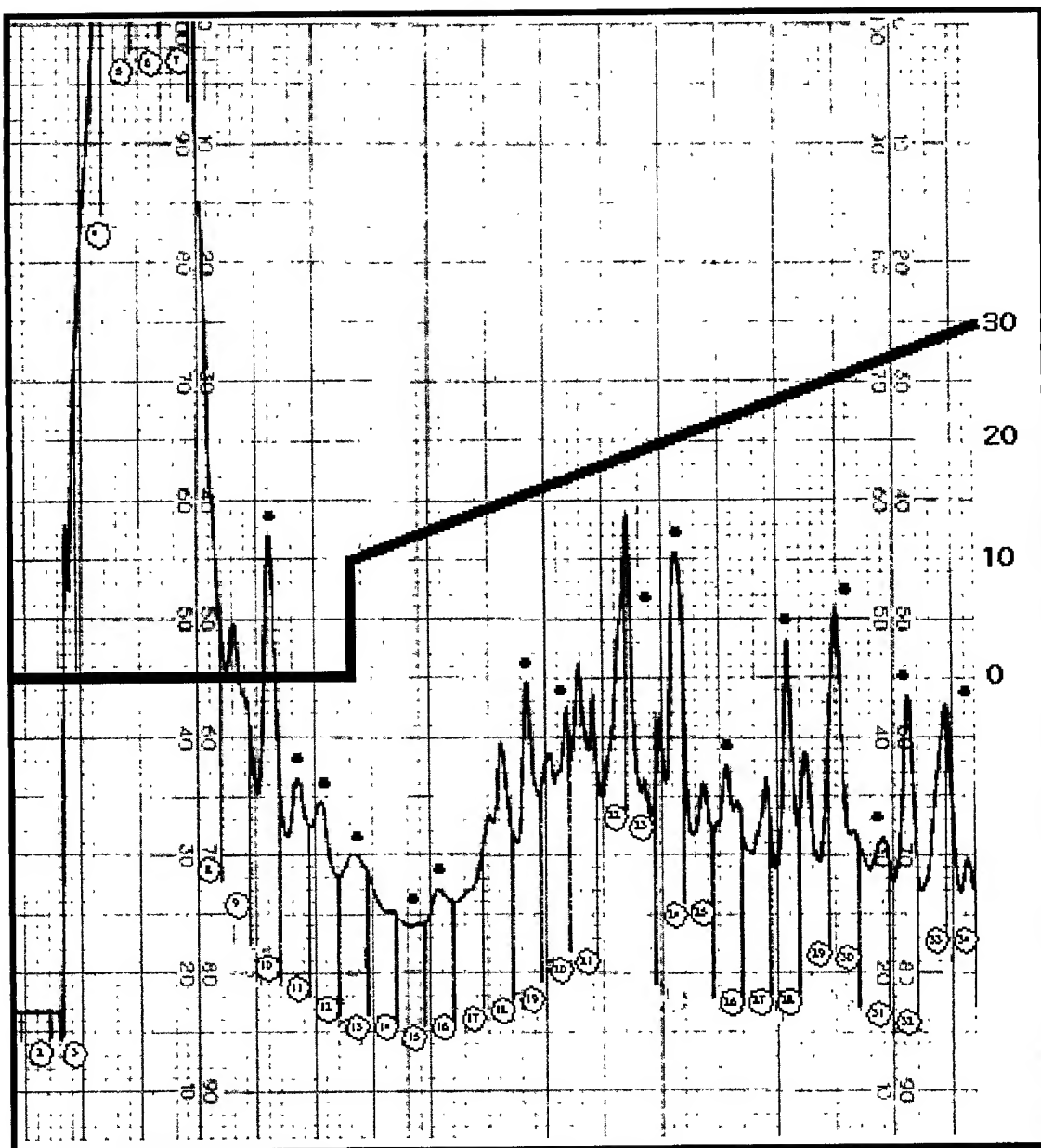


FIG. 17

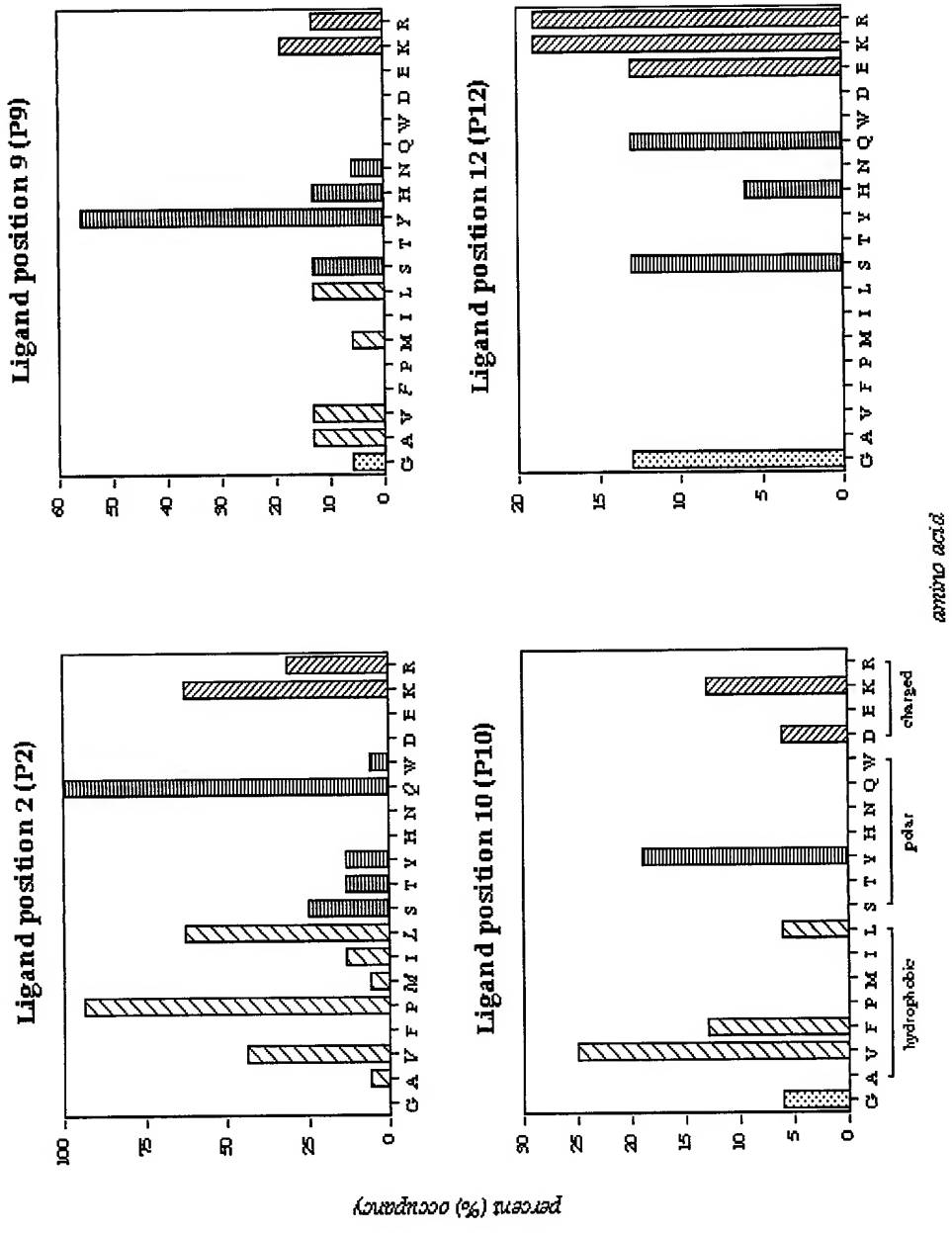


FIG. 18

Fraction 10											
	2	3	4	5	6	7	8	9	10	11	12
<i>dominant</i>	P	-	-	-	-	-	-	-	-	-	-
	Q										
<i>strong</i>	W	K	G	-	-	-	-	-	-	-	-
		R	F								
		H									
<i>weak</i>	S	E	D	S	H	V	I	Y	K	V	E
	I		N	W	S	T					
			M	P							
			I								

Fraction 15											
	2	3	4	5	6	7	8	9	10	11	12
<i>dominant</i>	P	-	-	-	-	-	-	-	-	-	-
	Q										
<i>strong</i>	W	K	G	-	-	-	-	-	-	-	-
		R	F								
		H									
<i>weak</i>	S	E	D	S	H	V	I	Y	K	V	E
	I		N	W	S	T					
			M	P							
			I								

Fraction 28											
position:	2	3	4	5	6	7	8	9	10	11	12
<i>dominant</i>	K	-	-	-	-	-	-	-	-	-	-
<i>strong</i>	Q	H	G	L	R	I	D	K	V	E	-
	V	N		S			N				
	P	R		H							
<i>weak</i>	-	P	E	P	V	P	Q	Y	-	F	S
		F		E	A	M	E	F		P	K
		K			F		A				
		D					H				
							W				

FIG. 19

FIG. 19
CONT'D.

Fraction 31										
posi tion:	2	3	4	5	6	7	8	9	1	0
<i>domi nant</i>	-	K	-	W	-	-	-	-	-	-
<i>strong</i>	S	H	N	R	S	F	-	G	F	
	Q			M	Y	V				
	P									
<i>weak</i>	L	Y	A	-	L	-	Y	Y	-	
		L			K		S			
		V					K			

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

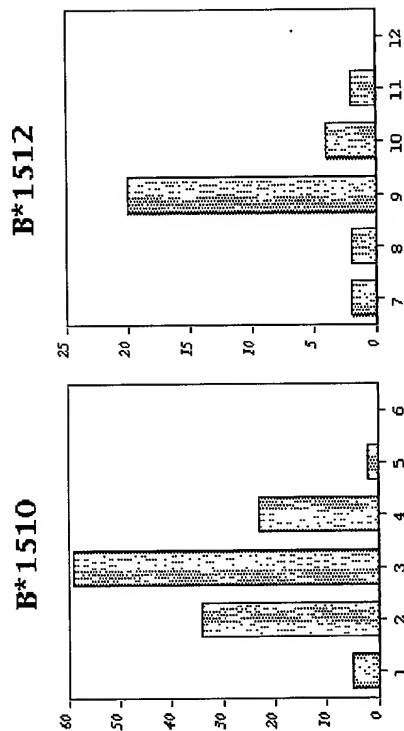
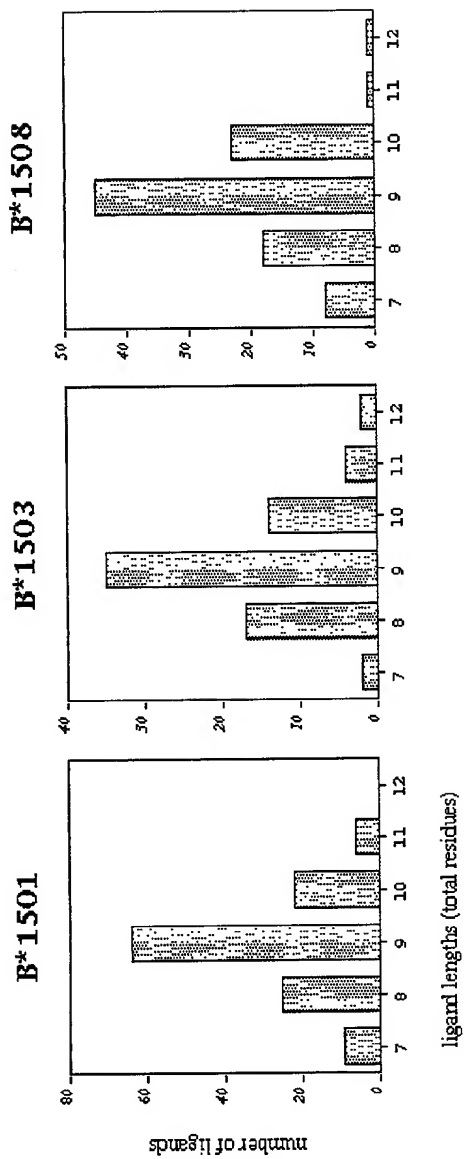


FIG. 20

B*1501

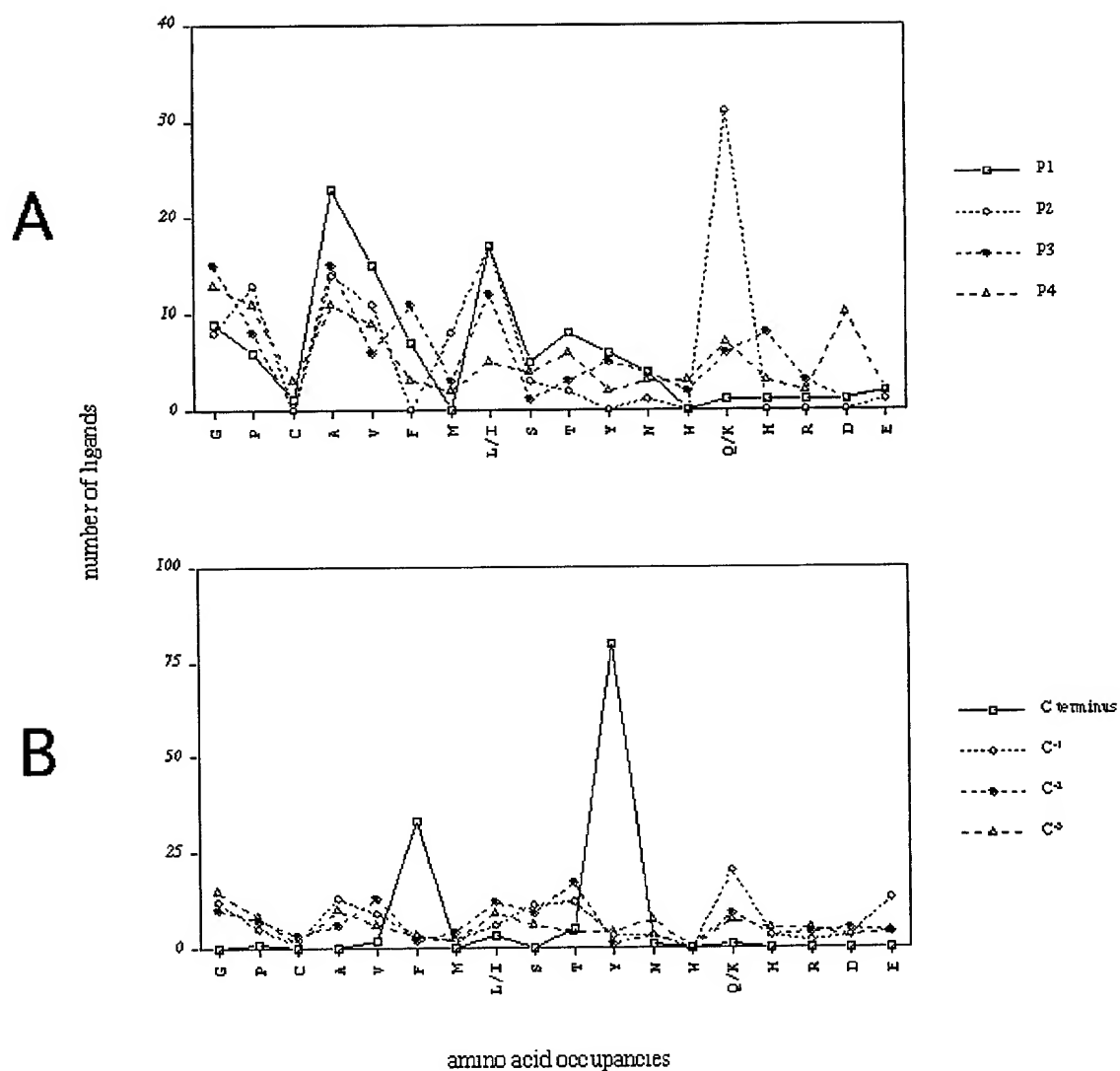
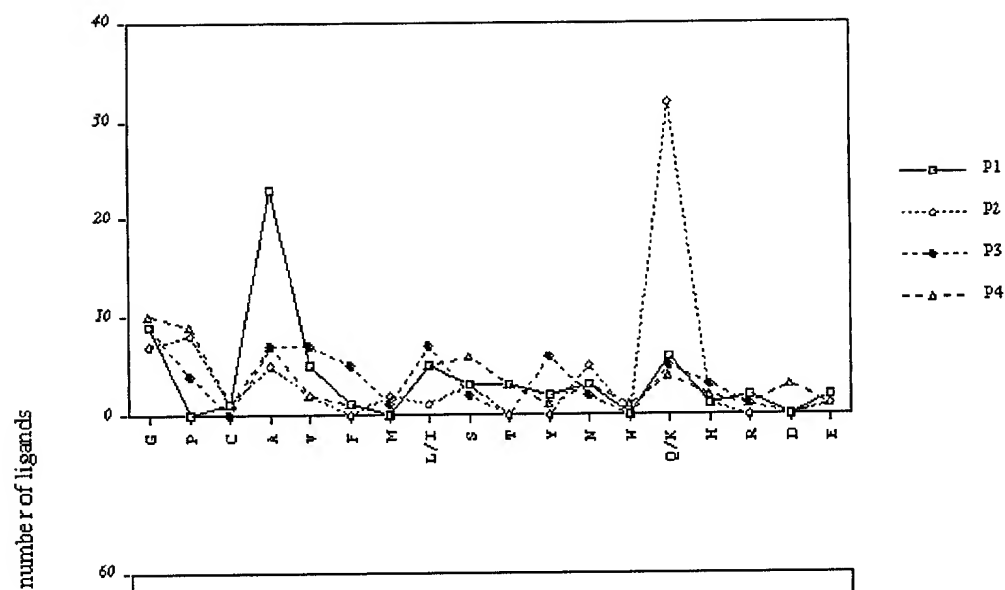


FIG. 21

B*1503

A



B

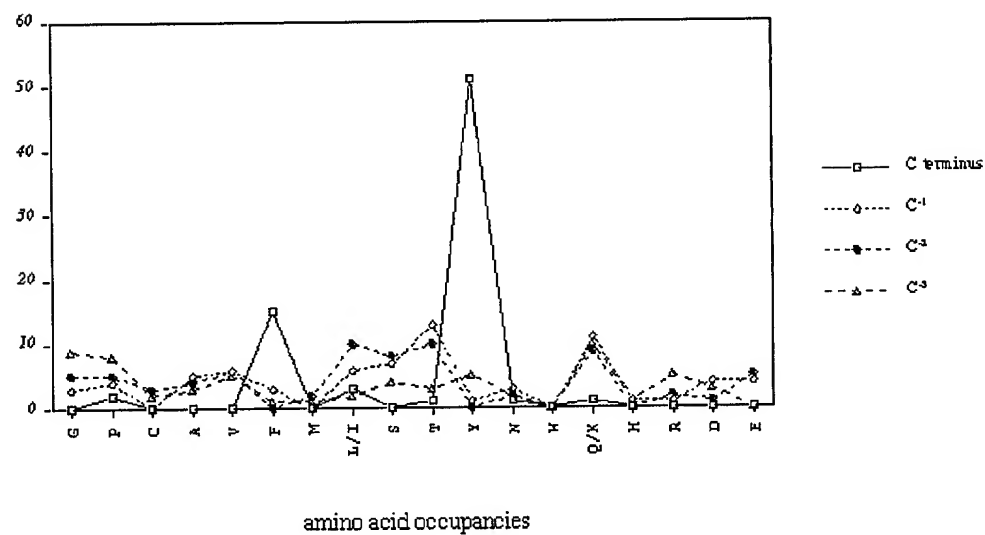
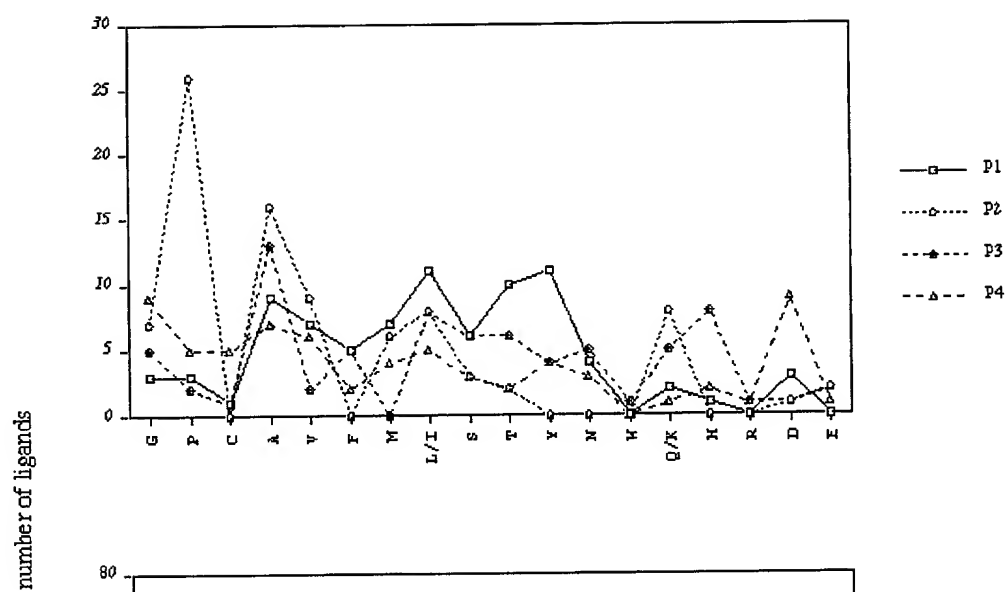


FIG. 22

B*1508

A



B

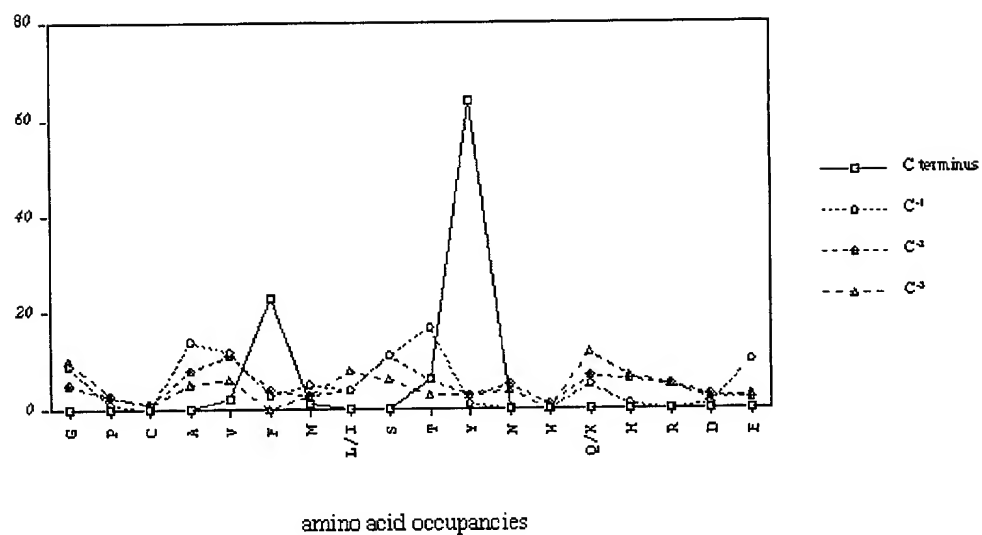
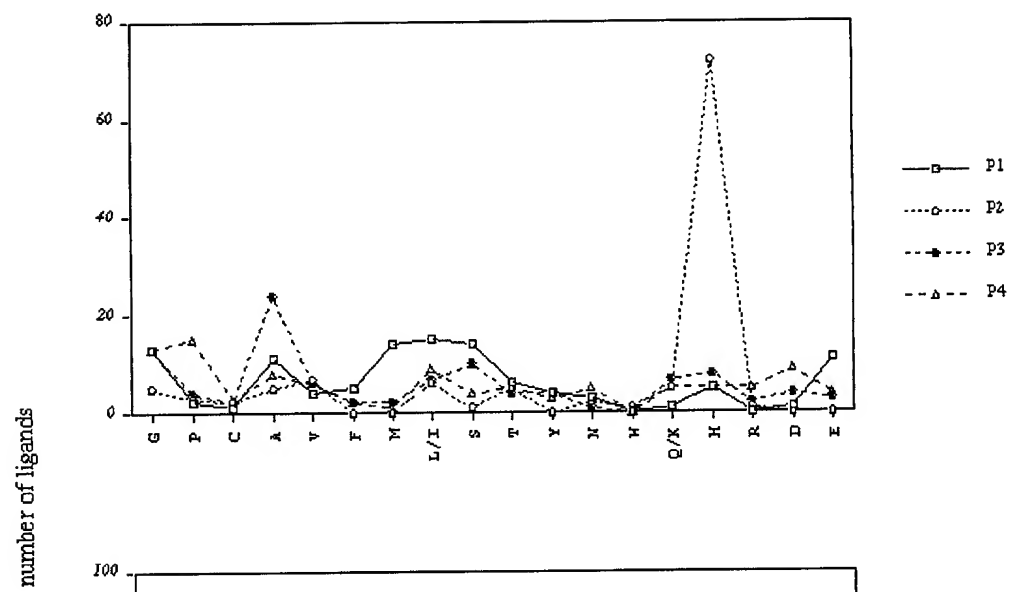


FIG. 23

B*1510

A



B

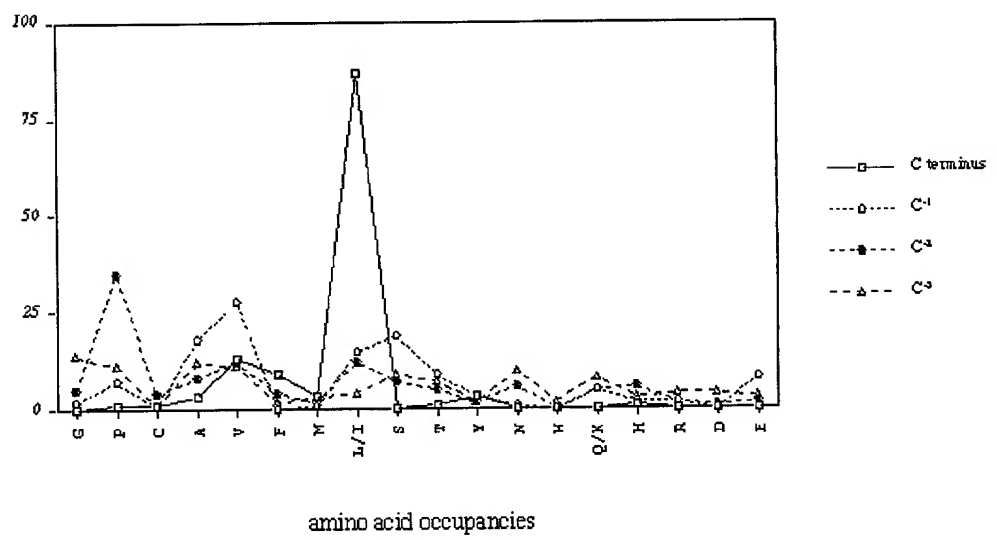
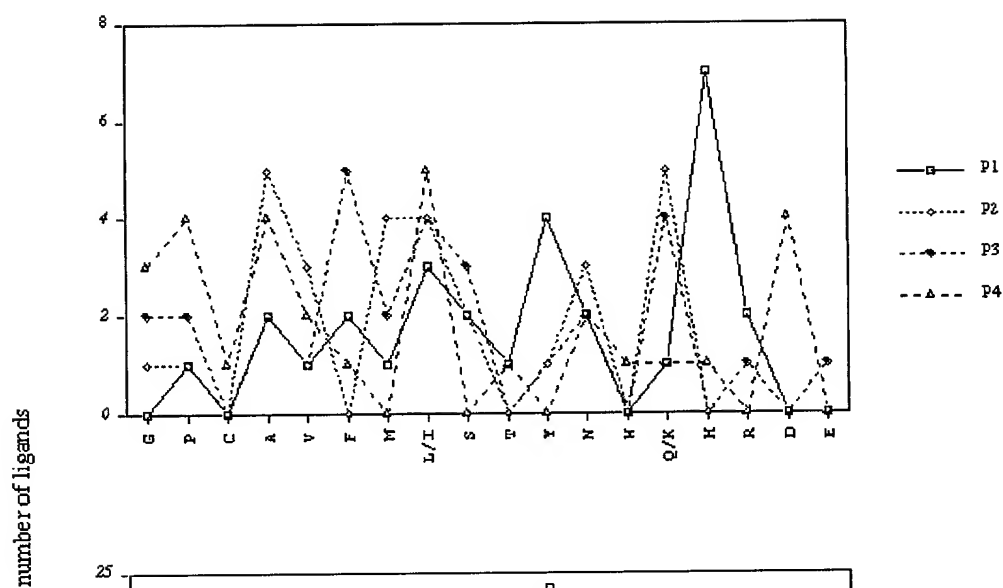


FIG. 24

B*1512

A



B

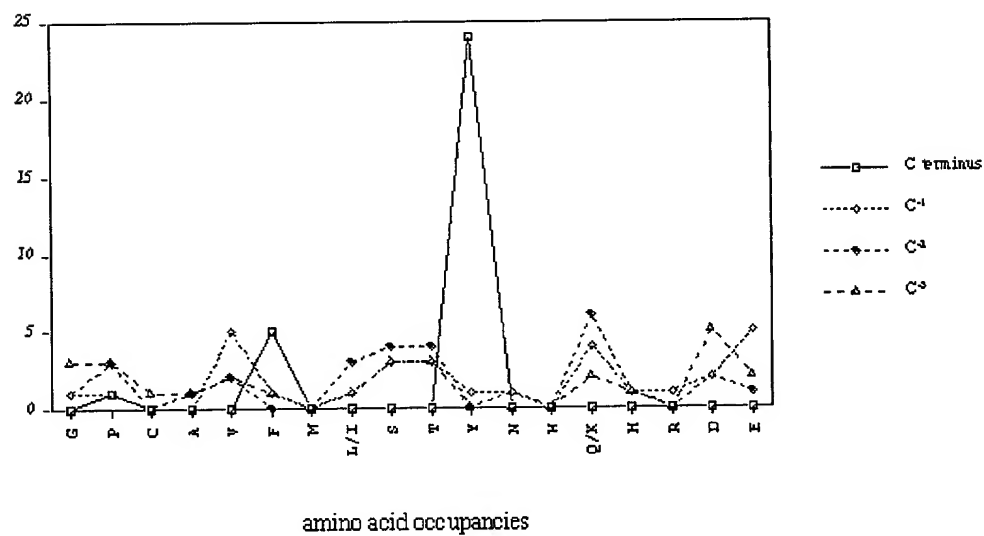
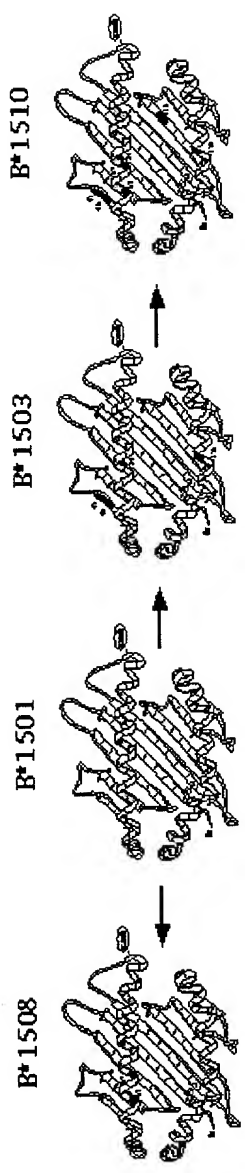


FIG. 25



--MDRHTXF	--MDRHTXF
-----YT	-----YT
GSFSGVAY	GSFSGVAY
TG-----AY	TG-----AY
FVSMHAY	FVSMHAY
SCFDHVTY	SCFDHVTY
XAM--VF	XAM--VF
FLZAMSTY	FLZAMSTY
TVXDSZTHY	TVXDSZTHY
VVACV----	VVACV----
FLA-N-HTY	FLA-N-HTY
VVAPITGY	VVAPITGY
FQAKXTY	FQAKXTY
VGVYDITGF	VGVYDITGF
-----XVEF	-----XVEF
TARXSVET	TARXSVET
AAFCG---XV	AAFCG---XV
YLN--ET	YLN--ET
ILGPPGSVY	ILGPPGSVY
XLGLWNW	XLGLWNW
YMLDPSGVSY	YMLDPSGVSY

NOZHGSAEY	NOZHGSAEY
TPXGEPVLSY	TPXGEPVLSY
SGFGGSGY	SGFGGSGY
CFLSCFT	CFLSCFT

ACFA SGAGZ	ACFA SGAGZ
-G--CDY	-G--CDY
APMARGZY	APMARGZY
GOZAVDF	GOZAVDF
MPAIZPN	MPAIZPN
-O-DEPPDMZY	-O-DEPPDMZY
GORXGAGSVF	GORXGAGSVF
AEFMACZY	AEFMACZY

FIG. 26

B*1508



1 2 3 4 5 6 7 8

B*1501



B*1503



FIG. 27

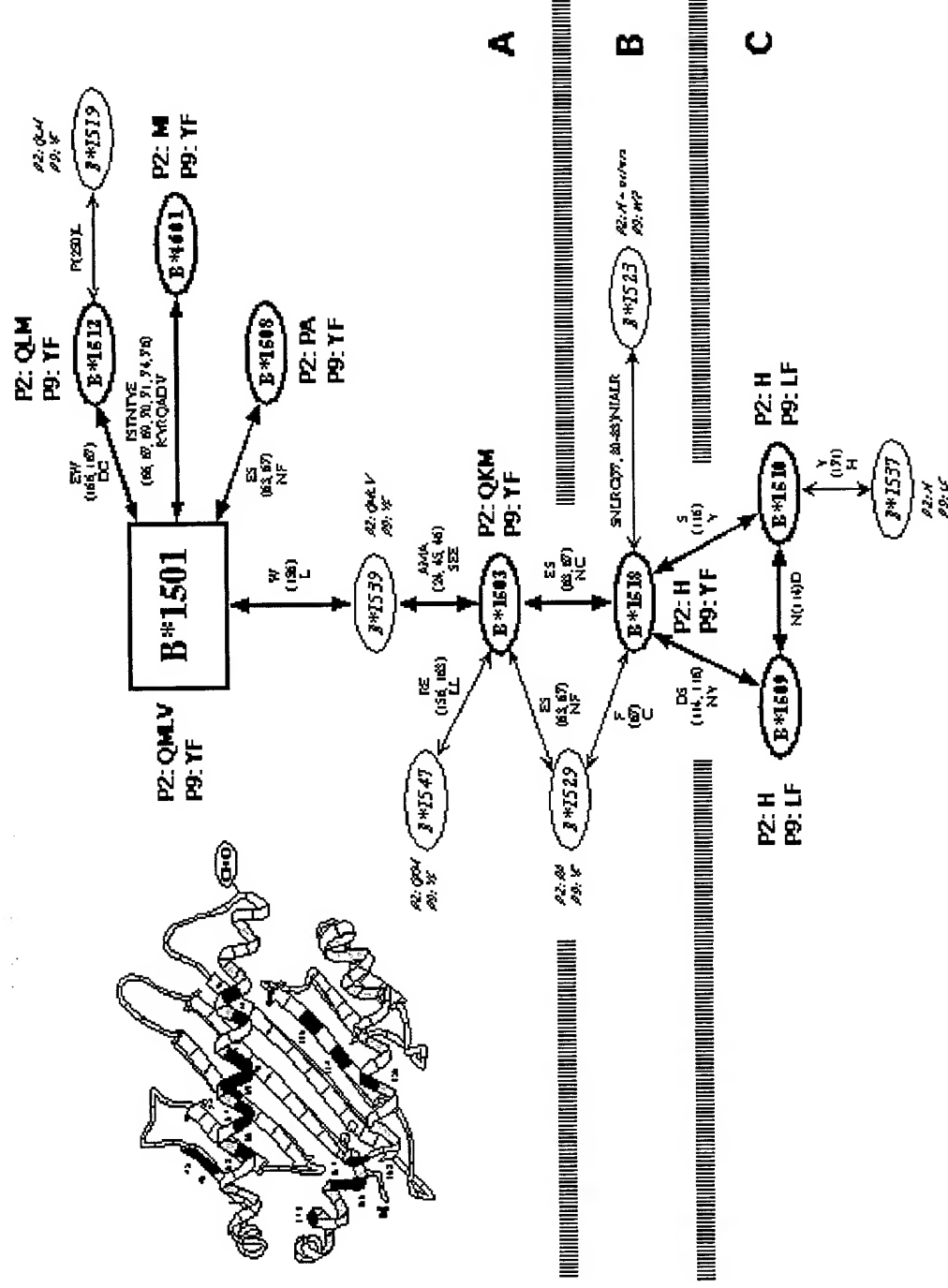
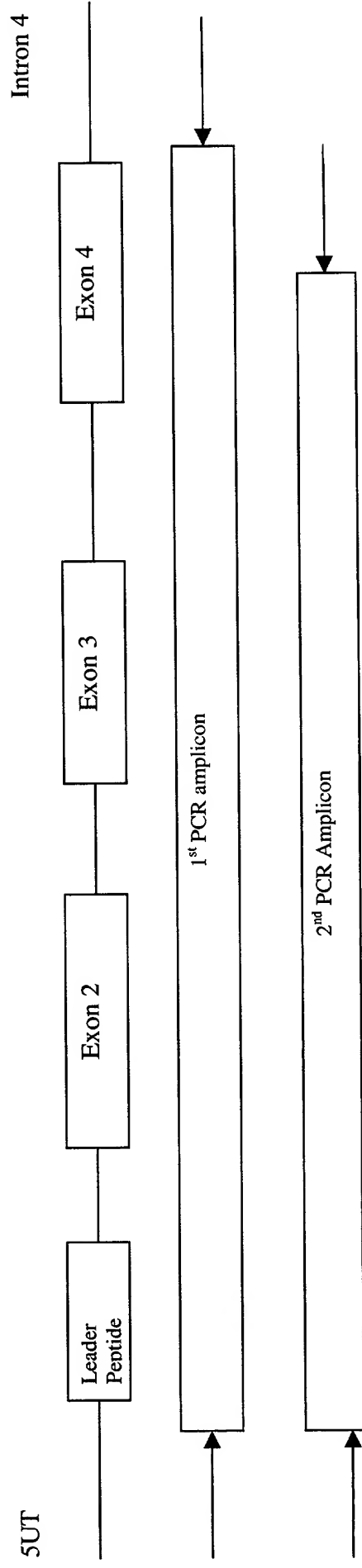


FIG. 28

FIG. 29 PCR Strategy



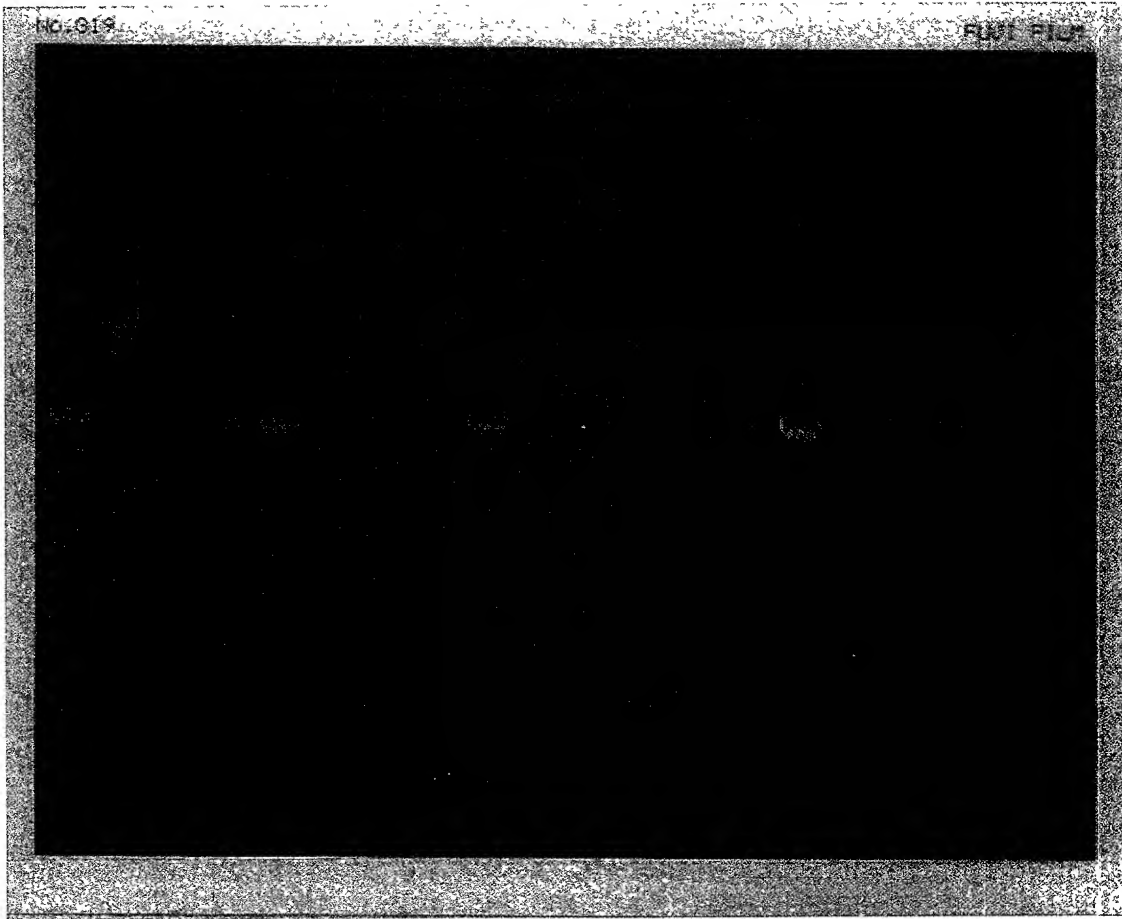


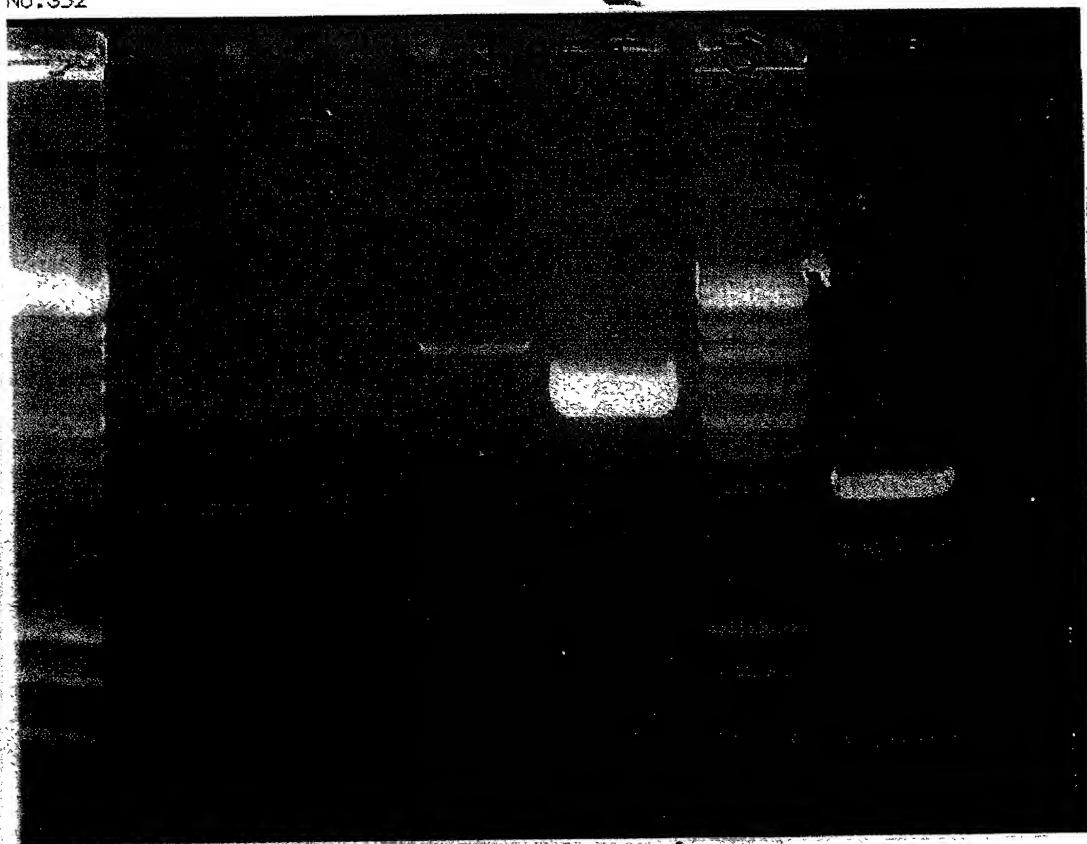
FIG. 30

The image is a dark, high-contrast, black and white scan, likely of a document page. It is predominantly black with some faint, illegible horizontal lines and shapes, suggesting text or figures that are not visible due to poor quality or damage. There are no discernible figures, tables, or text.

FIG. 31

No. 352

FUJI FILM



1 Hour 0.8% Gel

FIG. 32

GDNA FIG. 5

No. 368

3A394T PC1-12

FUJI FILM

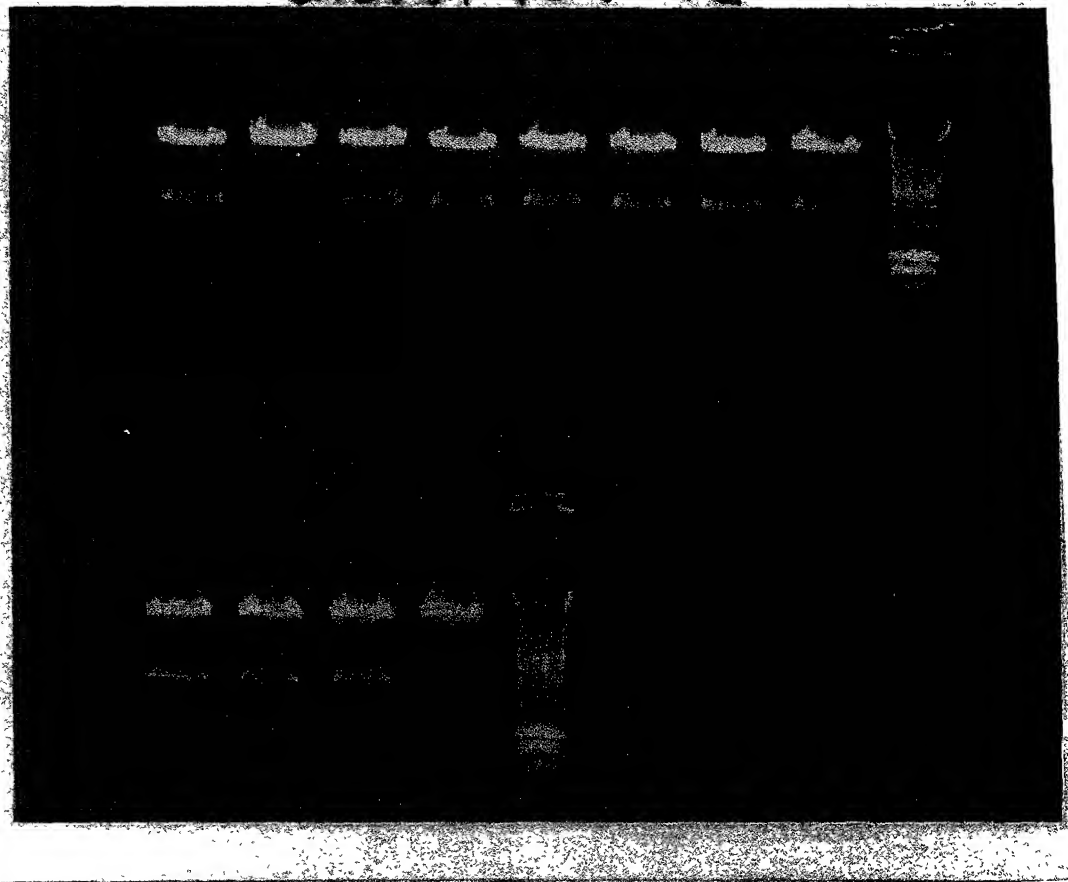


FIG. 33

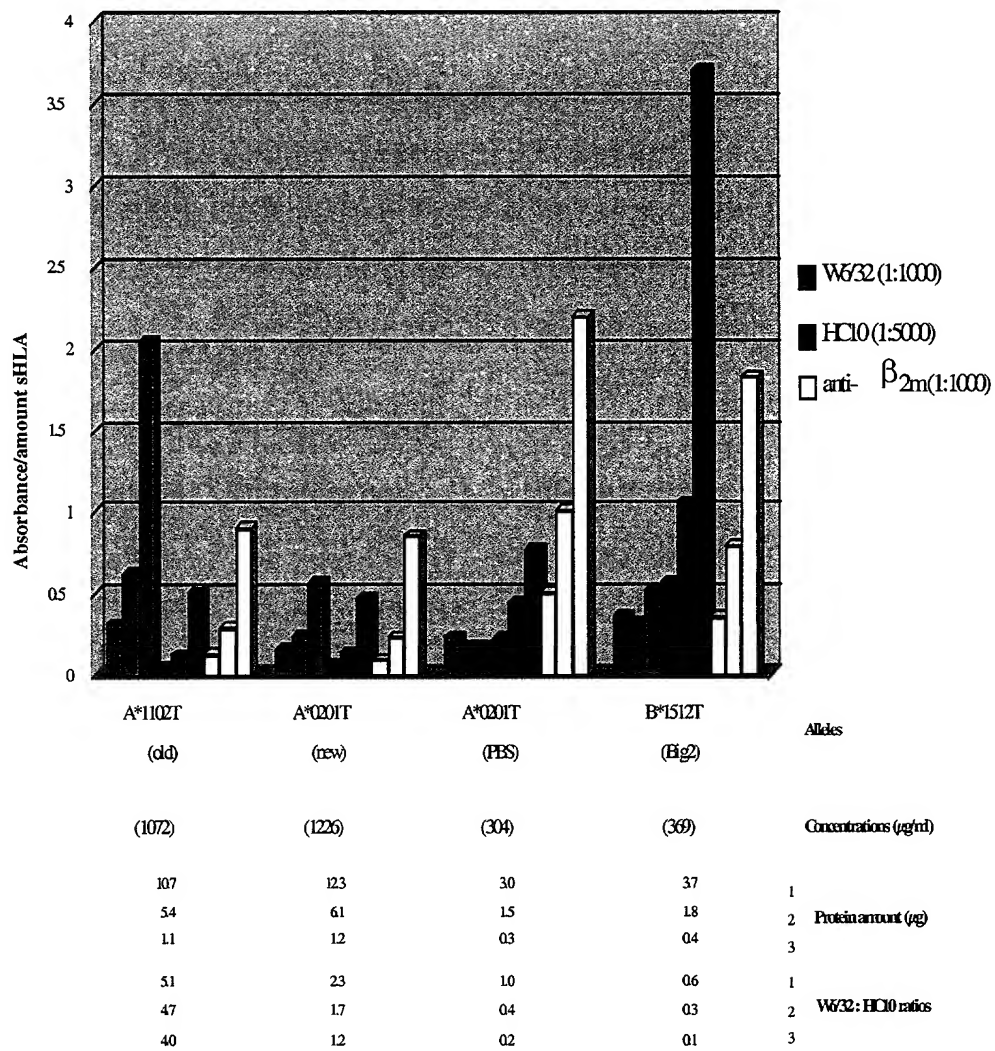


FIG. 34

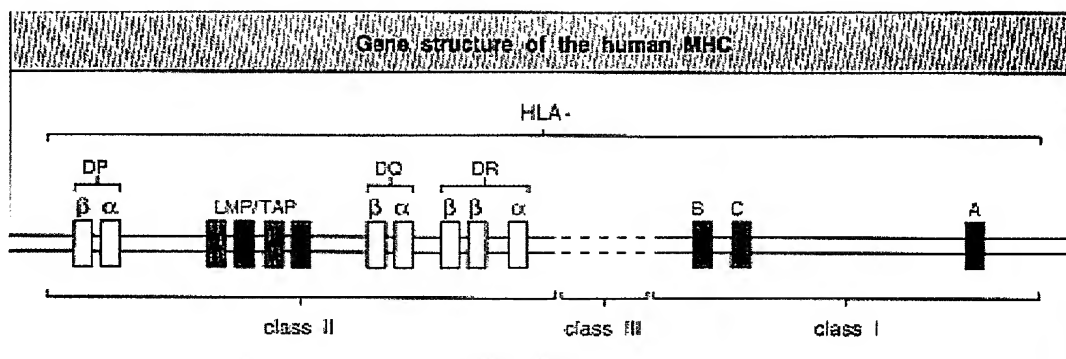


FIG. 35

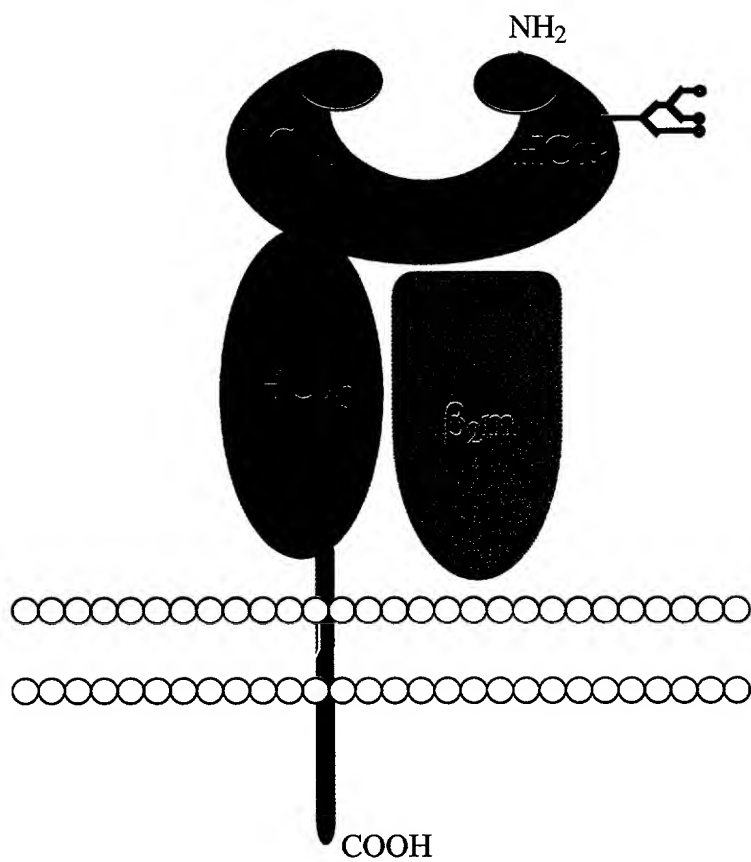


FIG. 36

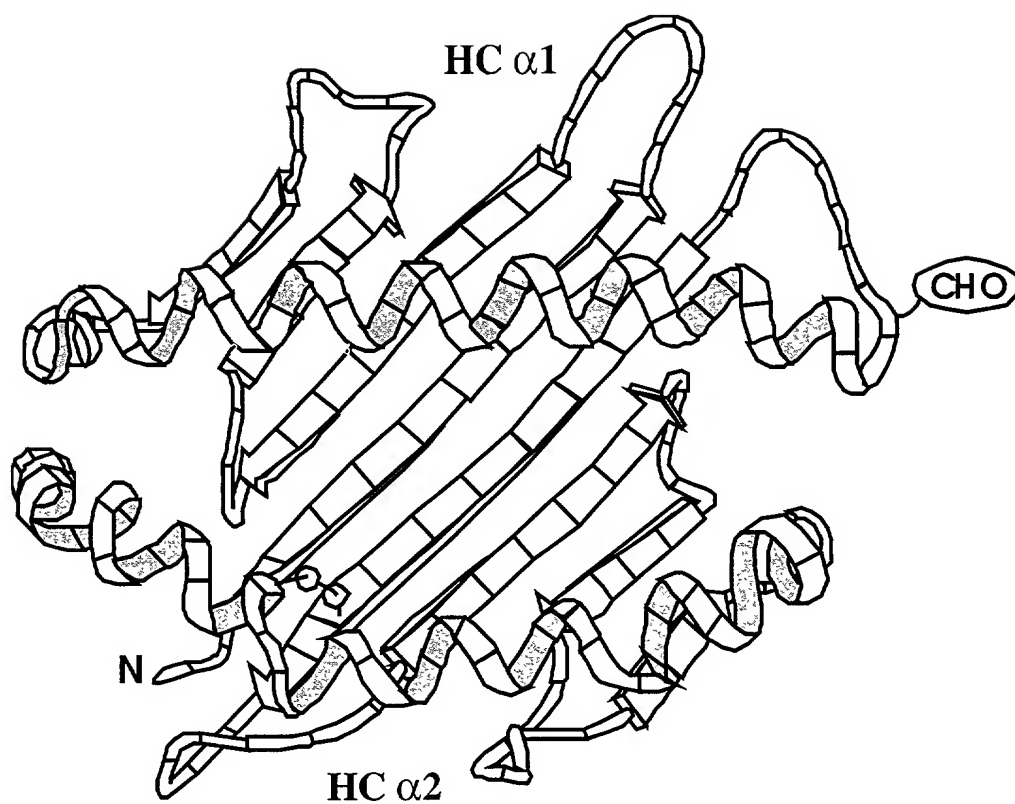


FIG. 37

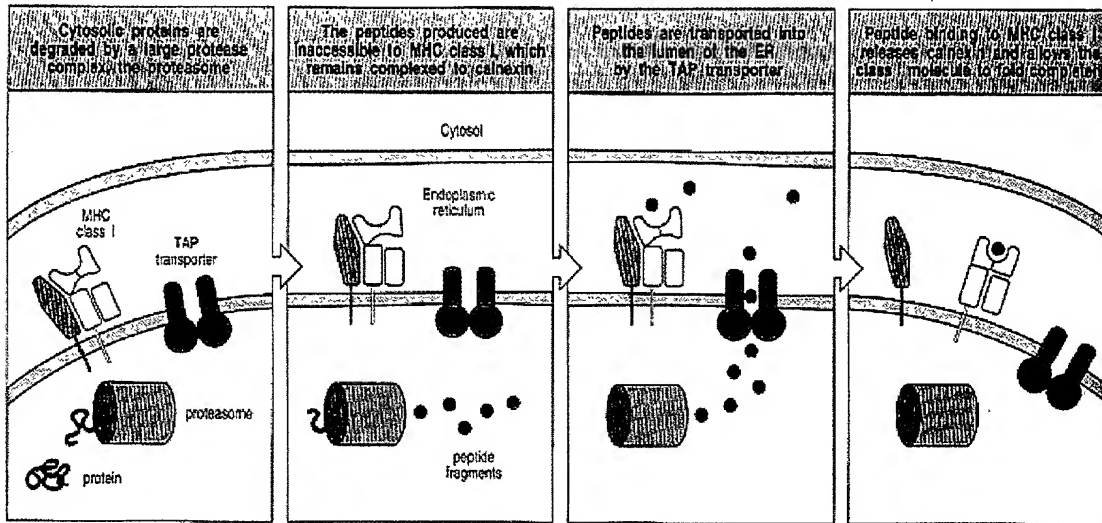


FIG. 38

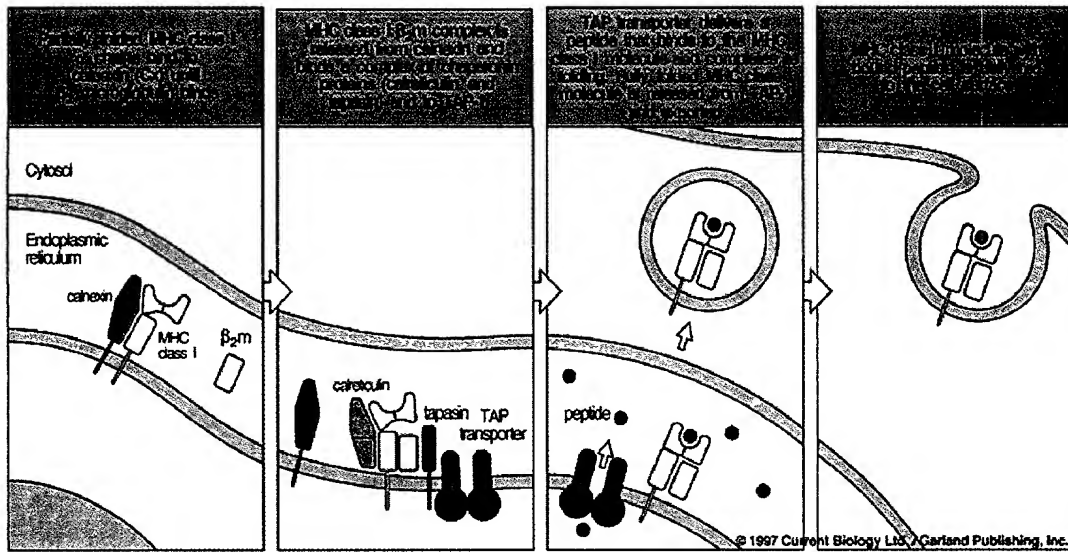


FIG. 39

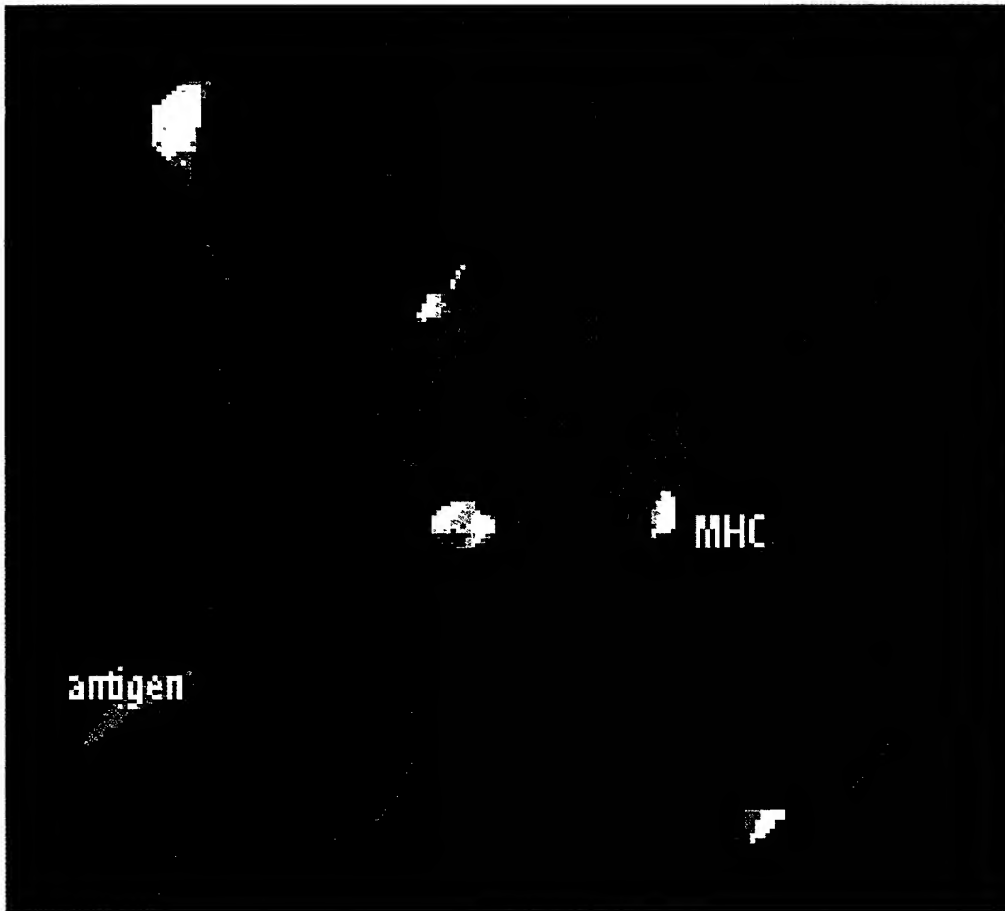


FIG. 40

FIG. 41

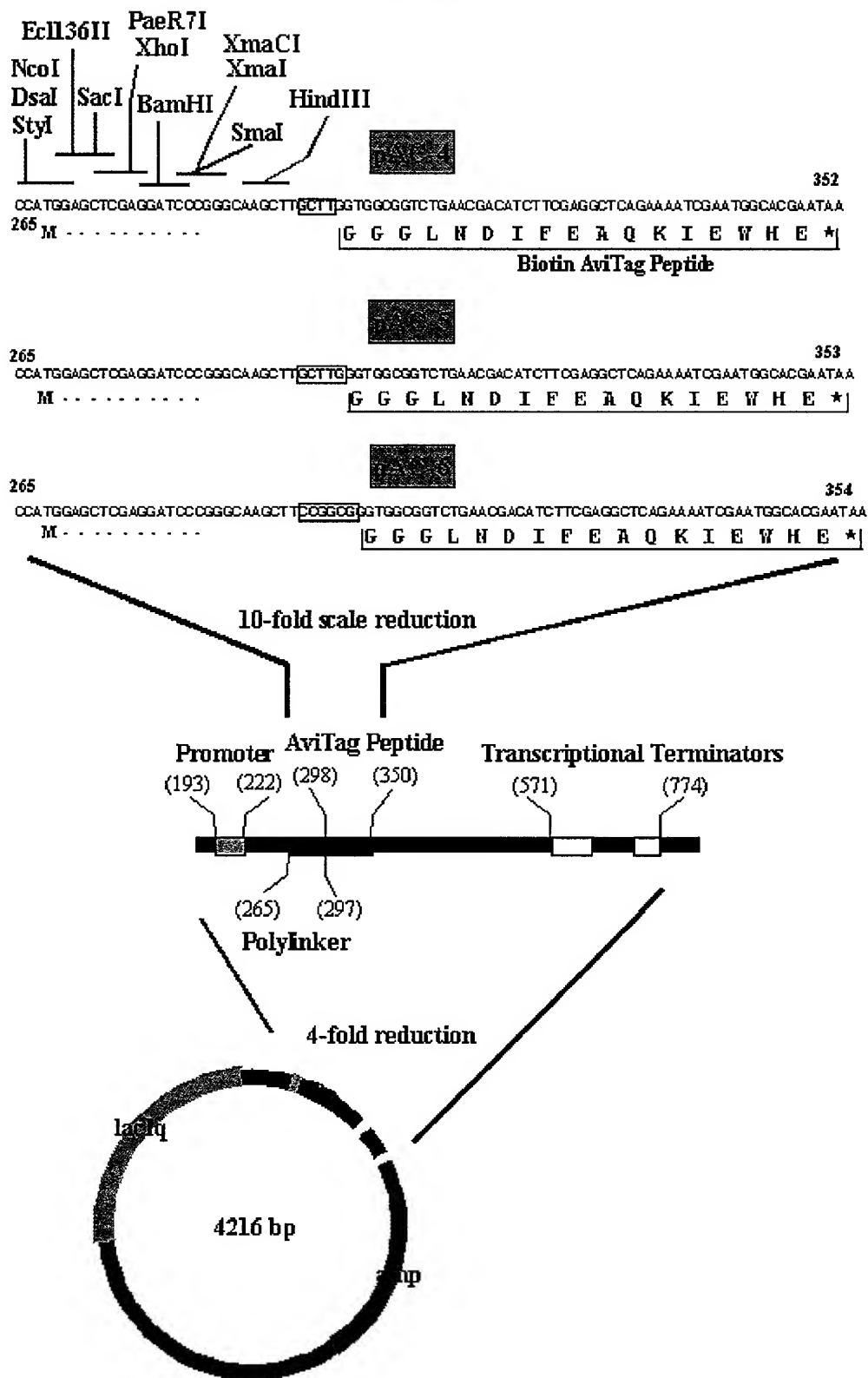




FIG. 42

SHLA-B*0702 PRODUCTION BY T2 TRANSFECTANTS AFTER PEPTIDE PULSING

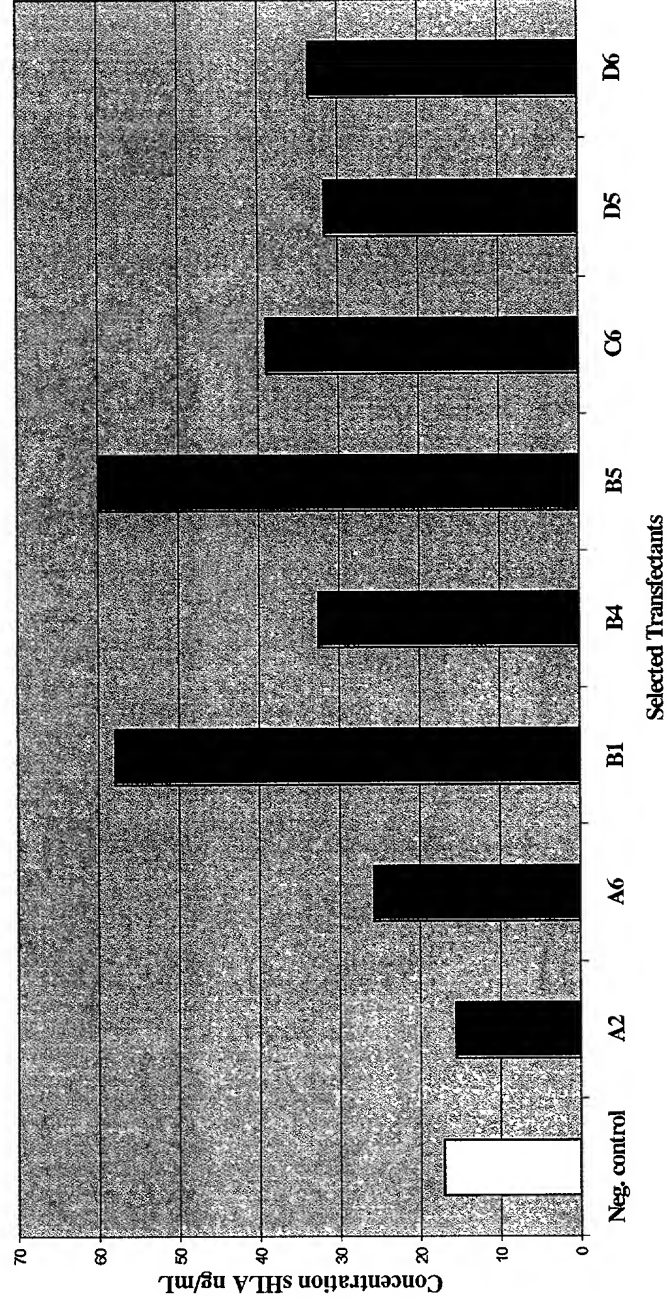


FIG. 44

sHLA Purification Elution Curve

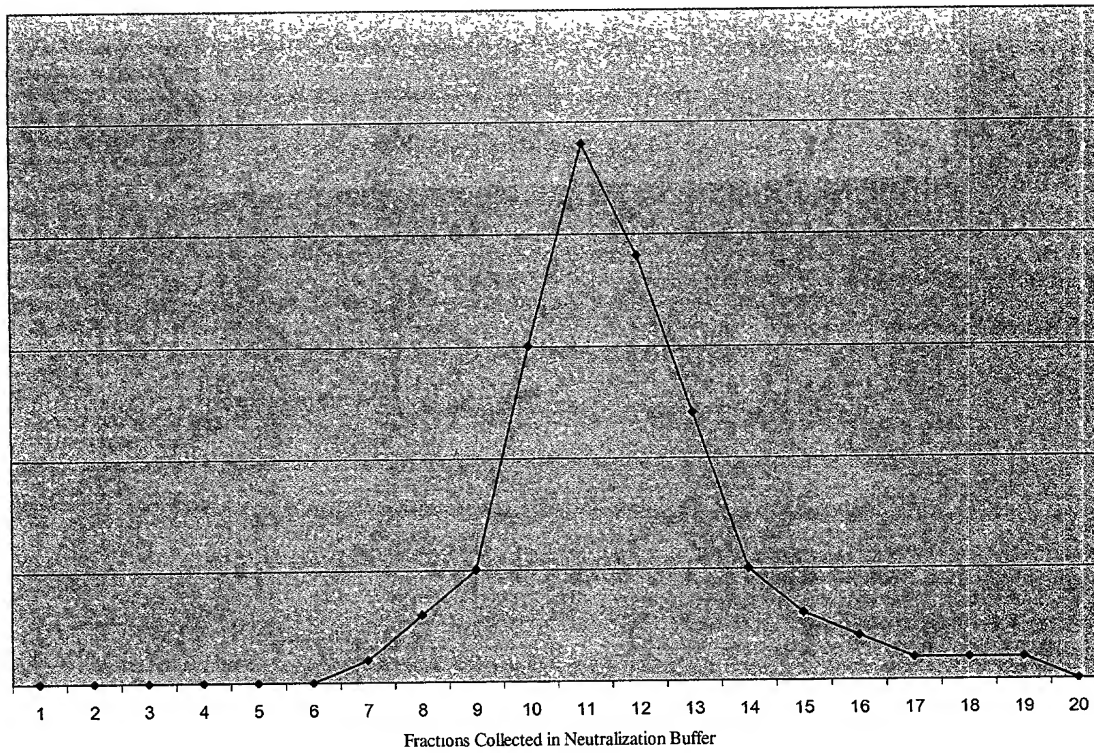


FIG. 45

ASSAY CONFIRMING BIOTINYLATION
Varying Reaction Times to Maximize Biotinylation Efficiency

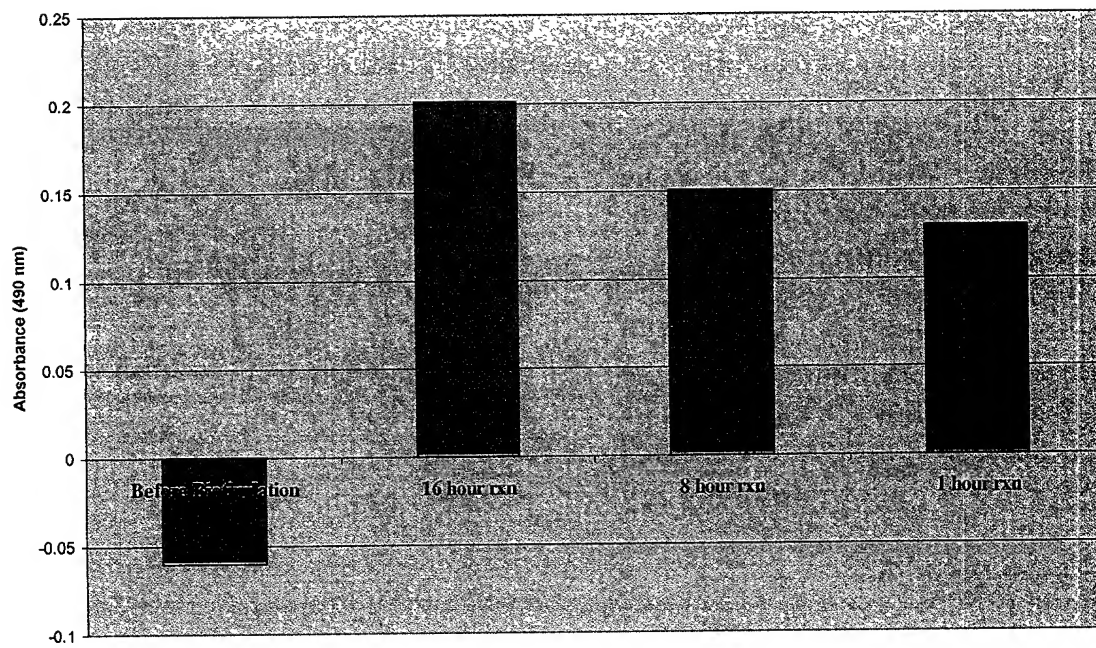


FIG. 46

SEPARATION OF BIOTINYLATED CLASS I FROM FREE BIOTIN

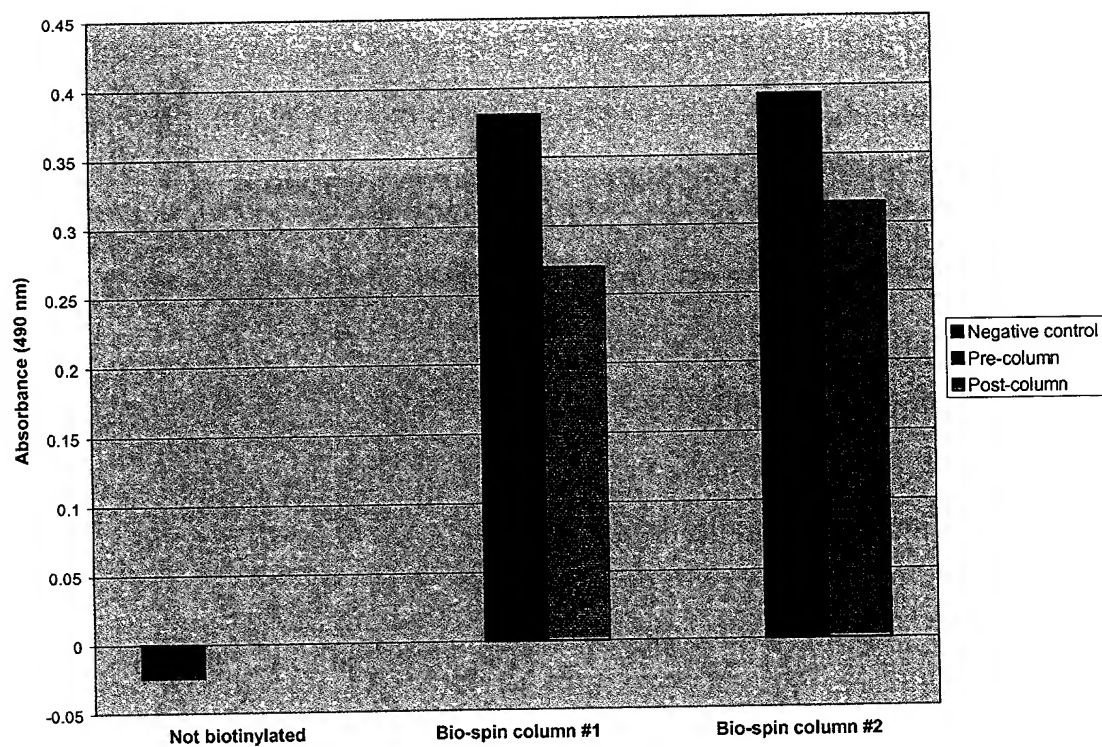


FIG. 47

	24	45	46	63	67	116	156	166	167	ethnicity
consensus	A	M	A	E	S	S	W	E	W	
B*1512	-	-	-	-	-	-	-	D	G	Thai
B*1508	-	-	-	N	F	-	-	-	-	Iranian/Indian/Amerindian
B*1501	-	-	-	-	-	-	-	-	-	Caucasian
B*1503	S	E	E	-	-	-	L	-	-	Black
B*1518	S	E	E	N	C	-	L	-	-	Indian
B*1510	S	E	E	N	C	Y	L	-	-	Black

TABLE 1

primer	type	sequence (5'→3')
HLA5UT	PCR (5'; inserts <i>SalI</i> site)	GGCGTCGACGGGACTCAGAATCTCCCCAGACGCCGAG
sHLA3TM	PCR (3'; inserts stop codon and <i>HindIII</i> site)	CCGCAAGCTTTCATCTCAGGGTGAG
5PXI	PCR (5'; inserts <i>XbaI</i> site)	GGGCTCTAGAGGACTCAGAATCTCCCCAGACGCCGAG
3PEI	PCR (3'; inserts stop codon and <i>EcoRI</i> site)	CCGCGAATTCATCTCAGGGTGAG
M13 universal	sequencing (mp18, end through α_3) (mp19, leader through α_2)	TGTAAAACGACGGCCAGT
3S	sequencing (α_2 through α_3)	CGGCAAGGATTACATCGCCCTG
JD3S	sequencing (α_3 through end)	CCCCATCGTGGGCAATCGTTG
3N	sequencing (α_2 through leader)	CAGGGCGATGTAATCCTTGCCG
4N	sequencing (α_3 through α_2)	GCCAGGTCAGTGTGATCTCCGC
T7 promoter	sequencing (T7 promoter forward priming site)	TAATACGACTCACTATAGGG
pcDNA3.1/BGH	sequencing (BGH reverse priming site)	TAGAAGGCACAGTCGAGG

TABLE 2

allele	# fractions	P2 extras	P9 extras	>9 cycles?
B*1501	7	P	-	yes (14)
B*1508	8	QVKRS	IVMQ	yes (14)
B*1503	3	P	MNL	yes (14)
B*1510	3	PR	MIY	yes (14)

TABLE 3

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

ligand	source protein	allele(s) characterized from
<i>HLA ligands</i>		
VGYVDDTQF	HLA-I α (49-57)	B*1501, 1508
IAVGYVDDTQF	HLA-I α (47-57)	B*1501, B*1512
IKADHVSTY	HLA-II DP α (32-40)	B*1503
GSHSMRYF	HLA-I α (25-32)	B*1503
<i>Replication/transcription/translation ligands</i>		
GQRKGAGSVF	60S ribosomal protein L8 (7-16)	B*1501, 1503
AQAESLRY	40S ribosomal protein S3 (100-107)	B*1501
GKVRTDITY	40S ribosomal protein S4 (73-81)	B*1503
SHAQTVVL	40S ribosomal protein S27 (48-55)	B*1510
SQFGGGSQY	eIF3-p66 (61-69)	B*1501, 1503, 1508, B*1512
VQGPVGTDF	zinc finger transcription factor (296-304)	B*1501
APPPPPPPP	transcription factor ZFM1 (581-589)	B*1501
YQHTGAVL	spleen mitotic checkpoint BUB3 (53-60)	B*1510
AHGRKMSKSL	valyl-tRNA synthetase (859-868)	B*1510
LPHQPLATY	Oct-binding factor 1 (52-60)	B*1508
AKYSTPATL	probable ATP-dependent RNA helicase DDX10 (280-288)	B*1503
AKAGITTTL	DNA replication licensing factor MCM5 (470-478)	B*1503
TQAPGNPVL	splicing factor U2AF large chain (179-187)	B*1510
SHQRQLLL	Kin17 (49-56)	B*1510
NQFQALLQY	polypyrimidine tract-binding protein (220-228)	B*1512
<i>Biosynthetic/degradative modification ligands</i>		
FVSNHAY	aldolase A (358-364)	B*1501, 1508
ILGPPGSVY	ubiquitin-protein ligase (83-91)	B*1501, B*1502, 1508, B*1512
YMIDPSGVSY	proteasome subunit C8 (150-159)	B*1501, B*1502, 1508, B*4601, B*1512
NHAIVSTSV	26S protease (S4) regulatory subunit (741-749)	B*1510
IHTPENPVI	lanosterol 14- α demethylase (488-496)	B*1510

TABLE 4

AHSNLA SVL	O-linked GlcNAc transferase (237-245)	B*1510
Signalling/modulatory ligands		
VVAPIT TGY	calcyclin binding protein (63-71)	B*1501, 1508
GHSPPT SSL	tyrosine-protein kinase JAK3 (491-499)	B*1510
LPPPPPP PP	Fas antigen ligand (54-62)	B*1503
NHANGL TL	serine/threonine protein phosphatase PP2A (α and β) (229-236)	B*1510
Transporter/chaperone ligands		
EHVASS PAL	13S Golgi transport complex 90 kD subunit (741-749)	B*1510
HHSDGS VSL	tapasin (354-362)	B*1509, B*1510
QPGPQ IVY	GABA/noradrenaline transporter (261-268)	B*1503
Structural/cytokinesis ligands		
NMNDLV SEY	tubulin β chain (414-422)	B*1508
THTQPG VQL	sepin 2 homolog (70-78)	B*1509, B*1510
SHANSA VVL	β -adaptin (249-257)	B*1509, B*1510
Unknown function ligands		
GQYPTQ PTY	KIAA0058 (5-13); like <i>Mus musculus</i> proline-rich protein	B*1503
VKVIQQ ESY	mammary tumor-associated protein INT6 (278-286)	B*1503
AKYPHV EDY	Ki nuclear autoantigen (207-215)	B*1503
AMNPTN TVF	heat shock cognate 71 kD protein (60-68)	B*1503
CPLSC FT	human HTGS database	B*1501, B*1503, B*1508
MPHSGY GF	human EST	B*1508
CHSAF AL	human HTGS database	B*1510
LHLLT LEA	human EST	B*1510
KNANLV QLY	human EST	B*1512

TABLE 4 CONT'D.

fraction	ion for MS/MS	derived peptide sequence
7	504.1 (+2)	H M S G Z P T S Y
7	549.2 (+2)	H N Z A A H Z E Y
8	526.0 (+2)	H A A X Y S Z V Y
10	484.3 (+2)	Y Q S D H R Y
11	424.3 (+2)	H X S T Z D F
11	464.3 (+2)	H A P P T D P P P
11	550.0 (+2)	H G P A N R D S V F
11	563.3 (+2)	F P Y P T D P Z Y
12	531.2 (+2)	Z N A N X V Z X Y
14	585.6 (+2)	R S F X X E N E Y
16	488.7 (+2)	H M Z N P T S Y
16	661.9 (+2)	Y V X F - - - V Y
17	577.6 (+2)	R S M X R C P E Y
18	523.0 (+2)	- - F Y T A Z T Y
20	582.4 (+2)	M Y N C N E X D Y
25	562.8 (+2)	N Q F Q A L L Q Y

TABLE 5

ALLELE	7	9	24	25	26	34	35	36	45	62	63	66	67	70	99	159	163	167	P2 MOTIF (dominant/str ong)
consensus	Y	Y	A	V	G	V	R	F	M	R	E	I	S	N	Y	Y	L	W	
B*1508	-	-	-	-	-	-	-	-	-	-	N	-	F	-	-	-	-	-	PA
B*1513	-	-	-	-	-	-	-	-	-	-	N	-	-	-	-	-	-	-	ILQVP
B*1502	-	-	-	-	-	-	-	-	-	-	N	-	-	-	-	-	-	-	LVQP
B*1501	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	QMLV
B*1512	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	QLM
B*1503	-	-	S	-	-	-	-	-	E	-	-	-	-	-	-	-	-	-	QXM
B*1518	-	-	S	-	-	-	-	-	E	-	N	-	C	-	-	-	-	-	H
B*1509	-	-	S	-	-	-	-	-	E	-	N	-	C	-	-	-	-	-	H
B*1510	-	-	S	-	-	-	-	-	E	-	N	-	C	-	-	-	-	-	H
B*1517	-	-	-	-	-	-	-	-	-	-	-	N	M	S	-	-	-	-	TS
B*1516	-	-	-	-	-	-	-	-	-	-	-	N	M	S	-	-	-	-	T
B*4601	-	-	-	-	-	-	-	-	-	-	-	K	Y	Q	-	-	-	-	MI

Table 6

ALLE LE	7 0	7 3	7 4	7 6	7 7	8 0	8 1	8 4	9 5	9 6	9 7	1 1	1 1	1 1	1 2	1 2	1 4	1 4	1 4	1 4	P9 MOTIF
																					(dominan t/strong)
<i>cons ensu s</i>	N	T	Y	E	S	N	L	Y	L	Q	R	D	S	Y	Y	I	I	T	K	W	
B*1 502	-	-	-	-	-	-	-	-	I	-	-	-	-	-	-	-	-	-	-	-	YFM
B*1 501	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	YF
B*1 503	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	YF
B*1 508	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	YF
B*1 512	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	YF
B*1 518	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	YF
B*4 601	Q	-	D	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	YF
B*1 517	S	-	-	-	N	I	A	-	-	-	-	H	D	-	-	-	-	-	-	-	YF
B*1 516	S	-	-	-	N	I	A	-	W	-	-	-	-	-	-	-	-	-	-	-	Y
B*1 509	-	-	-	-	-	-	-	-	-	-	-	N	Y	-	-	-	-	-	-	-	LF
B*1 510	-	-	-	-	-	-	-	-	-	-	-	-	Y	-	-	-	-	-	-	-	LF
B*1 513	-	-	-	-	N	I	A	-	I	-	-	-	-	-	-	-	-	-	-	-	W

TABLE 7

fraction	ion for MS/MS	derived peptide sequence
9	490.3 (+2)	A G G Z P A T P P A X
9	513.1 (+2)	S H Z G C V Z P A V
10	433.8 (+2)	G H D P D S P A A
10	455.4 (+2)	E H V A S S P A L
10	482.6 (+2)	M C Z - G M P A X
10	482.8 (+2)	G H G A N N D P A X
10	495.7 (+2)	X H S Z P A G P A X
11	448.9 (+2)	M H A D N P V X
11	482.8 (+2)	G H <u>C</u> P R N P A X
11	495.7 (+2)	X H S G A P Z A P X
11	516.7 (+2)	X H D T <u>E</u> H A P X
12	448.4 (+2)	T Q A P G N P V L
12	460.3 (+2)	T Z A <u>G</u> <u>C</u> M V P X
13	464.8 (+2)	M V - - H P V X
14	456.7 (+2)	A H S V P S P A F
14	477.7 (+2)	M H T - - P A P V
14	482.8 (+2)	P G A A V V P S X
15	510.1 (+2)	I H T P E N P V I
16	456.7 (+2)	S H <u>D</u> <u>G</u> <u>S</u> V P T X
16	522.7 (+2)	- - - - - P V X
16	523.3 (+2)	M A H S - - P V F
17	523.2 (+2)	- H - - - - P V F
18	474.8 (+2)	M X <u>G</u> <u>X</u> S F P A X
18	491.2 (+2)	V H T C V N P V X
18	515.8 (+2)	E W <u>H</u> <u>Y</u> P V S X
19	496.6 (+2)	<u>E</u> T P E H A P V X

TABLE 8

side chain	P1	P2	P3	P4	C ¹	C ²	C ³	C-term	side chain
G	-	-	11.90%	10.32%	11.90%	-	-	-	G
P	-	10.32%	-	-	-	-	-	-	P
C	-	-	-	-	-	-	-	-	C
A	18.25%	11.11%	11.90%	-	-	-	10.32%	-	A
V	11.90%	-	-	-	10.32%	-	-	-	V
F	-	-	-	-	-	-	26.19%	-	F
M	-	-	-	-	-	-	-	-	M
I/L	13.49%	13.49%	-	-	-	-	-	-	I/L
S	-	-	-	-	-	-	-	-	S
T	-	-	-	-	13.49%	-	-	-	T
Y	-	-	-	-	-	-	-	63.49%	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	24.60%	-	-	-	-	15.87%	-	Q/K
H	-	-	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	-	-	-	-	-	D
E	-	-	-	-	-	-	10.32%	-	E
N value	13.64	19.52	3.80	0.32	1.90	3.81	6.51	69.68	C value
N _{sum}	37.28				81.90				C _{sum}
	B*1501 N _{sum} /C _{sum} = 0.46								

TABLE 9

1990 2000 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100

side chain	P1	P2	P3	P4	C ⁻³	C ⁻²	C ⁻¹	C-term	side chain
G	12.16%	-	12.16%	13.51%	12.16%	-	-	-	G
P	-	10.81%	-	12.16%	10.81%	-	-	-	P
C	-	-	-	-	-	-	-	-	C
A	31.08%	-	-	-	-	-	-	-	A
V	-	-	-	-	-	-	-	-	V
F	-	-	-	-	-	-	-	20.27%	F
M	-	-	-	-	-	-	-	-	M
I/L	-	-	-	-	-	13.51%	-	-	I/L
S	-	-	-	-	-	10.81%	-	-	S
T	-	-	-	-	-	13.51%	17.57%	-	T
Y	-	-	-	-	-	-	-	68.92%	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	43.24%	-	-	13.51%	12.16%	14.86%	-	Q/K
H	-	-	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	-	-	-	-	-	D
E	-	-	-	-	-	-	-	-	E
N value	23.24	34.05	2.16	5.67	6.48	9.99	12.43	69.19	C value
N _{sum}	65.12				98.09				C _{sum}
B*1503 N _{sum} /C _{sum} = 0.66									

TABLE 10

side chain	P1	P2	P3	P4	C ³	C ²	C ¹	C-term	side chain
G	-	-	-	-	10.42%	-	-	-	G
P	-	27.08%	-	-	-	-	-	-	P
C	-	-	-	-	-	-	-	-	C
A	-	16.67%	13.54%	-	-	-	14.58%	-	A
V	-	-	-	-	-	11.46%	12.50%	-	V
F	-	-	-	-	-	-	-	23.96%	F
M	-	-	-	-	-	-	-	-	M
I/L	11.46%	-	-	-	-	-	-	-	I/L
S	-	-	-	-	-	11.46%	11.46%	-	S
T	10.42%	-	-	-	-	-	17.71%	-	T
Y	11.46%	-	-	-	-	-	-	66.67%	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	-	-	-	12.50%	-	-	-	Q/K
H	-	-	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	-	-	-	-	-	D
E	-	-	-	-	-	-	10.42%	-	E
N value	3.34	23.75	3.54	0.00	2.92	2.92	16.67	70.63	C value
N _{sum}	30.63				93.14				C _{sum}
					B*1508 N _{sum} /C _{sum} = 0.33				

TABLE 11

side chain	P1	P2	P3	P4	C ¹	C ²	C ³	C-term	side chain
G	10.57%	-	10.57%	10.57%	-	-	11.38%	-	G
P	-	-	-	12.20%	-	28.46%	-	-	P
C	-	-	-	-	-	-	-	-	C
A	-	-	19.51%	-	-	-	-	14.63%	A
V	-	-	-	-	-	-	-	22.76%	V
F	-	-	-	-	-	-	-	-	F
M	11.38%	-	-	-	-	-	-	-	M
I/L	12.20%	-	-	-	-	-	-	12.20%	I/L
S	11.38%	-	-	-	-	-	-	15.45%	S
T	-	-	-	-	-	-	-	-	T
Y	-	-	-	-	-	-	-	-	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	-	-	-	-	-	-	-	Q/K
H	-	58.54%	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	-	-	-	-	-	D
E	-	-	-	-	-	-	-	-	E
N value	5.53	48.54	10.08	2.77	1.38	18.46	25.04	61.3	C value
N _{sum}	66.92				106.18				C _{sum}
B*1510 N _{sum} /C _{sum} = 0.63									

TABLE 12

side chain	P1	P2	P3	P4	C ³	C ²	C ¹	C-term	side chain
G	-	-	-	-	-	-	-	-	G
P	-	-	-	13.33%	-	-	-	-	P
C	-	-	-	-	-	-	-	-	C
A	-	16.67%	-	13.33%	-	-	-	-	A
V	-	-	-	-	-	-	16.67%	-	V
F	-	-	16.67%	-	-	-	-	16.67%	F
M	-	13.33%	-	-	-	-	-	-	M
I/L	-	13.33%	13.33%	16.67%	-	-	-	-	I/L
S	-	-	-	-	-	13.33%	-	-	S
T	-	-	-	-	-	13.33%	-	-	T
Y	13.33%	-	-	-	-	-	-	80.00%	Y
N	-	-	-	-	-	-	-	-	N
W	-	-	-	-	-	-	-	-	W
Q/K	-	16.67%	13.33%	-	-	20.00%	13.33%	-	Q/K
H	23.33%	-	-	-	-	-	-	-	H
R	-	-	-	-	-	-	-	-	R
D	-	-	-	13.33%	16.67%	-	-	-	D
E	-	-	-	-	-	-	16.67%	-	E
N value	16.66	20.00	13.33	16.66	6.67	16.66	16.67	76.67	C value
N _{sum}	66.65				116.67				C _{sum}
B*1512 N _{sum} /C _{sum} = 0.57									

TABLE 13

fraction	ion for MS/MS	derived peptide sequence	alleles overlapping
6	398.2 (+3)	- - W D R H T X F	B*1501/B*1508
6	448.2 (+2)	- - - - - Y T	B*1501/B*1508
7	418.7 (+2)	A Q F A S G A G Z	B*1501/B*1503
8	402.2 (+2)	- G - - C D Y	B*1501/B*1503
8	418.7 (+2)	G S H F G V A Y	B*1501/B*1508
8	516.7 (+2)	N Q Z H G S A E Y	B*1501/B*1503/B*1508/B*1512
8	642.7 (+2)	P M N D W X M T Z T Y	B*1501/B*1512
9	331.4 (+3)	A P M A R G Z Y	B*1501/B*1503
9	418.7 (+2)	F V S N H A Y	B*1501/B*1508
9	433.2 (+2)	N P P A Z Z P N	B*1501/B*1503
9	437.0 (+2)	T G - - - - A Y	B*1501/B*1508
9	441.2 (+2)	- Q - D P P P D M Z Y	B*1501/B*1503
9	446.6 (+2)	G Q Z Z A V D F	B*1501/B*1503
9/10	465.2 (+2)	S Q F G G G S Q Y	B*1501/B*1503/B*1508/B*1512
9	476.2 (+2)	S Q F D H V T Y	B*1501/B*1508
9	578.0 (+2)	T P X G E P Y Z S Y	B*1501/B*1503/B*1508
10	398.3 (+2)	X A N - - V T	B*1501/B*1508
10	456.8 (+2)	C P L S C F T	B*1501/B*1503/B*1508
10	509.0 (+2)	F L Z A M Z S T Y	B*1501/B*1508/B*1512
10	532.0 (+2)	T V X D S Z T H Y	B*1501/B*1508/B*1512
13	503.6 (+2)	G Q R K G A G S V F	B*1501/B*1503
14	460.7 (+2)	V V A P I T T G Y	B*1501/B*1508
14	475.1 (+2)	V V A C V - - - Y	B*1501/B*1508
14	525.3 (+2)	P L A - N - H T Y	B*1501/B*1508
15	514.2 (+2)	F Q A R X T E Y	B*1501/B*1508
16	522.0 (+2)	V G Y V D D T Q F	B*1501/B*1508
17	351.3 (+3)	A A F C G - - - X V	B*1501/B*1508
17	408.7 (+2)	Y L H - - E T	B*1501/B*1508
17/18	451.4 (+2)	I L G P P G S V Y	B*1501/B*1508/B*1512
17	462.4 (+2)	X L G D V N M Y	B*1501/B*1508
17	507.0 (+2)	- - - - X V E F	B*1501/B*1508
17	519.2 (+2)	T A R V X S V E Y	B*1501/B*1508
18	565.7 (+2)	A E F W A C Z X Y	B*1501/B*1503
18/19	566.2 (+2)	Y M I D P S G V S Y	B*1501/B*1508/B*1512
19/20	560.0 (+2)	X V E X T T D Y Y	B*1501/B*1512
20/21	448.2 (+2)	A A G X G P T F Y	B*1501/B*1512
20/21	614.0 (+2)	I A V G Y V D D T Q F	B*1501/B*1512
21/22	507.2 (+2)	V A E V X F V G Y	B*1501/B*1512
21/22	557.2 (+2)	Y N R W S X E F	B*1501/B*1512
22/23	510.8 (+2)	A L M P - - X N Y	B*1501/B*1512

TABLE 14

allele	ion overlaps collided	positive overlaps	overlap frequency
B*1512	20	14	70%
B*1508	286	25	9%
B*1503	88	12	14%
B*1510	26	0	0%

TABLE 15

motif P2/P9		+ length variation only	+ P2 variation only		
DLASMLNRY	(64-72)	QMLLCVF	(1-7)	DIEGHASHY	(28-36)
MLNRYKLIY	(68-76)	HLDIEGHASHY	(26-36)	SAPLEKQLF	(123-131)
PLEKQLFYY	(125-133)	MLSAPLEKQLF	(121-131)	APLEKQLFY	(124-132)
YQLRCHLSY	(149-157)	PLEKQLF	(125-131)	LPNTRPHSY	(138-146)
ALSINGDKF	(159-167)	PLEKQLFY	(125-132)	NTRPHSYVF	(140-148)
DLPDLRGPF	(203-211)	TMLPNTRPHSY	(136-146)	SINGDKFQY	(161-169)
FVPNLKDMF	(242-250)	MLPNTRPHSY	(137-146)	YTGAMTSKF	(169-177)
AVTMTAASY	(253-261)	QLRCHLSY	(150-157)	TSKFLMGTY	(174-182)
TMFEVSVAF	(290-298)	YVALSINGDKF	(157-167)	L TSAQSGDY	(216-224)
DLRWLAKSF	(314-322)	FQYTGAMTSKF	(167-177)	YSLVIVTTF	(224-232)
HLTTEKQEY	(366-374)	AMTSKFLMGTY	(172-182)	VIVTTFVHY	(227-235)
ALRLATVGY	(375-383)	HVLSLVF	(192-198)	TTFVHYANF	(238-246)
ALGTESGLF	(467-475)	SLTSAQSGDY	(215-224)	MTAASYARY	(256-264)
AVSNAVDGF	(505-513)	SLVIVTTF	(225-232)	DTETLTTF	(284-292)
ALYEASTTY	(564-572)	LVIVTTF	(226-232)	ATVKGMQSY	(338-346)
RQIPKIQNF	(597-605)	IVTTFVHY	(228-235)	ATSVLLSAY	(396-404)
ILSSNYFDF	(643-651)	IVTTFVHYANF	(228-238)	SAYNRHPLF	(402-410)
TVMEIAGLY	(666-674)	FVHYANFHNH	(232-241)	HTVMRETLF	(414-422)
HVVLAILLY	(679-687)	FVHYANFHNFY	(232-242)	ESGLFSPCY	(471-479)
VVLAILLYF	(680-688)	TMTAASY	(255-261)	SPCYLSLRF	(476-484)
FLVHKIVMF	(696-704)	TMTAASYARY	(255-264)	IIPLINVTF	(544-552)
LVHKIVMFF	(697-705)	ELDTETLTTF	(282-292)	TTYLSSSLF	(570-578)
		TMFEVSVAFF	(290-399)	NSILSSNYF	(641-649)
		TVLKDIIGICY	(326-326)	AILLYFIAF	(683-691)
		VLKDIIGICY	(327-326)	FIAFALGIF	(688-696)
		TVKGMQSY	(339-346)		
		RLATVGY	(377-383)		
		TVGYPKAGVY	(380-389)		
		LLSAYNRHPLF	(400-410)		
		PLHTVMRETLF	(412-422)		
		VMRETLF	(416-422)		
		GLALGTESGLF	(465-475)		
		GLFSPCY	(473-479)		
		LMIIPLINVTF	(542-552)		
		PLINVTF	(546-552)		
		EVGRSALY	(559-566)		
		YLSSSLF	(572-578)		
		TQKSCIF	(608-614)		
		TQKSCIFCGF	(608-617)		
		GLETTTY	(627-633)		
		VQNSILSSNY	(639-648)		
		VQNSILSSNYF	(639-649)		
		ILSSNYF	(643-649)		
		VMEIAGLY	(667-674)		
		VVLAILLY	(680-687)		
		VVLAILLYF	(680-688)		
		VLAILLY	(681-687)		
		VLAILLYF	(681-688)		
		VLAILLYFIAF	(681-691)		
		ILYFIAF	(685-691)		
		FLVHKIVMFF	(696-705)		

TABLE 16

TABLE 17

Primer name	Sequence 5'-3'	Locus	Cut site	Annealing site
PP5UTA	GCGCTCTAGACCCAGACGCCGAGGATGGCC	A	XbaI	5UT
3PI4A	GCCCTGACCCCTGCTAAAGGT	A		Intron 4
PP5UTB	GCGCTCTAGACCAACCCGGACTCAGAAATCTCCT	B	XbaI	5UT
3PI4B	TGCTTTCCCTGAGAAAGAGAT	B		Intron 4
5UTB39	AGGCGAATTCCAGAGTCTCCTCAGACGCG	B*39	EcoRI	5UT B39
5PKCE	GGGCGAATTCCCGCCGCCACCATGCGGGTCATGGCGCC	C	EcoRI	5UT
3PI4C	TTCTGCTTTCTGAGAAAGAC	C		Intron 4
PP5UT	GGGCGAATTCCGGACTCAGAAATCTCCCCAGACGCCGAG	B	EcoRI	5UT
PP3PEI	CCGCGAATTCTCATCTCAGGGTGAGGGCT	A,B,C	EcoRI	Exon 4
PP3PEIH	CCGCAAGCTTTTCATCTCAGGGTGAGGGCT	A,B,C	HindIII	Exon 4
3PEIHC7	CCGCAAGCTTTTCAGCTCAGGGTGAGGGCT	Cw*07	HindIII	Exon 4

Primer Name	Sequence 5'-3'
T7Prom	TAATACGACTCACTATAGGG
BGHrev	TAGAAGGCACAGTCGAGG
PPI2E2R	GTCGTGACCTGCGCCCC
PPI2E2F	TTTCATTTTCAGTTTAGGCCA
ABCI3E4F	GGTGTCTCTGTCCATTCTCA

5'CY5 Sequencing Primers

TABLE 18

TABLE 19

Sample	OD 260nm	OD 280nm	260nm/280nm	Dilution factor	Concentration ug/ml
3A394	0.0346	0.0202	1.7111	20	34.5821

TABLE 20

Sample	OD 260nm	OD 280nm	260nm/280nm	Dilution factor	Concentration ug/ml
3A394TPC 1	0.2821	0.1505	1.8739	20	282.0960

bioRxiv preprint doi: <https://doi.org/10.1101/2021.04.14.438888>; this version posted April 14, 2021. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

TABLE 21

Sample	OD 260nm	OD 280nm	260nm/280nm	Dilution factor	Concentration ug/ml
3A394TPC 1	0.6919	0.3625	1.9087	50	1729.8492

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

TABLE 22

Sample	Decay time milliseconds	# live cells/ml	# dead cells/ml	Viability %
3A394TPC 1	19.8	1.12×10^6	1.65×10^5	87.16

TABLE 23

Sample	Optical Density 492nm	Dilution	Concentration of soluble HLA ng/ml
3A394TP C1 well 1	1.278 1.388 (over range)	1.0	247.270
3A394TP C1 well 2	1.227 1.274	1.0	229.855
3A394TP C1 well 3	1.021 1.042	1.0	154.403
3A394TP C1 well 4	1.108 1.070	1.0	169.001

TABLE 24

Allele	Allele Allele AlleleConcentration by ELISA ug/ml	Concentration by ELISA ug/ml Concentration by ELISA ug/ml Concentration by ELISA ug/mlTotal amount made mg
<u>Total amount made mg</u> <u>Total amount made mg</u> <u>Total amount made mg</u> HLA- A*0301	545.4	3.47
HLA-A*1102	888.5	2.57
HLA-A*2902	476.8	2.58
HLA-A*3002	50.3	3.38
HLA-A*3201	1382.0	9.61
HLA-A*3301	40.0	0.8
HLA-B*0801	66.0	21.0
HLA-B*1302	55.0	9.0
HLA-B*1401	146.0	50.0
HLA-B*1801	587.6	0.4
HLA-B*3701	1831.0	119.0
HLA-B*3801	128.0	66.0
HLA-B*3905	1400.0	120.0
HLA-B*40012	59.0	10.0
HLA-B*4002	400.0	180.0
HLA-B*4101	288.4	8.8
HLA-B*4402	59.0	10.0

TABLE A

fraction	ion for MS/MS	derived peptide sequence
6	398.2 (+3)	- - W D R H T X F
6	448.2 (+2)	- - - - - Y T
7	382.7 (+2)	V Q F E A A T
7	418.7 (+2)	A Q F A S G A G Z
7	455.2 (+2)	A L G A - - R G Y
7	489.1 (+2)	- - V - - G H X Y
7	506.8 (+2)	X S - - - C E Y
8	402.2 (+2)	- G - - C D Y
8	419.2 (+2)	G S H F G V A Y
8	433.8 (+2)	A P P P P P P P P
8	455.2 (+2)	- - - Z A R G Y
8	462.2 (+2)	D P H A P P Z Y
8	507.2 (+2)	A V P S X H X X Y
8	512.3 (+2)	X A Z V Z M T A Y
8	512.8 (+2)	A L N G R V T M Y
8	516.9 (+2)	N Q Z H G S A E Y
8	522.9 (+2)	F G X A C X A T S Y
8	642.7 (+2)	P M N D W X M T Z T Y
9	331.4 (+3)	A P M A R G Z Y
9	418.7 (+2)	F V S N H A Y
9	426.2 (+3)	- - - - - - - - S Y
9	433.3 (+2)	N P P A Z Z P N
9	437.0 (+2)	T G - - - - A Y
9	441.2 (+3)	- Q - D P P P D M Z Y
9	446.6 (+2)	G Q Z Z A V D F
9	453.6 (+2)	X Q - - A G G Z Y
9	465.2 (+2)	S Q F G G G S Q Y
9	476.2 (+2)	S Q F D H V T Y
9	481.0 (+2)	G Q H A S V X S Y
9	514.2 (+2)	- - A A H V P P G Y
9	550.2 (+2)	F M D V G A P T V Y
9	578.0 (+2)	T P X G E P Y Z S Y
10	398.3 (+2)	X A N - - V T
10	448.2 (+2)	A Q A A P F A G Y
10	448.4 (+2)	V V V F G V Z F
10	450.4 (+2)	A Q M - - S E Y
10	456.8 (+2)	C P L S C F T
10	464.7 (+2)	- - - - F G H Y
10	473.7 (+2)	A L W - - P Z F
10	486.4 (+2)	V P H Z N A Y

TABLE A CONT'D.

10	498.7 (+2)	- - - - - G H G G Y
10	509.0 (+2)	F L Z A M Z S T Y
10	527.7 (+2)	G Q Y V V Z P T Y
10	532.0 (+2)	T V X D S Z T H Y
10	540.2 (+2)	P M F D P P Z T F
11	469.2 (+2)	A Q A E S L R Y
11	480.6 (+2)	X A V G H S G G T Y
11	511.2 (+2)	- - - - - P T Y
11	516.7 (+2)	E S X P N N V P Y
12	383.0 (+3)	L A H T E C P R G Y
12	435.0 (+2)	- - - - - P S Y
12	473.2 (+2)	V Q G P V G V Q Y
12	475.0 (+2)	R G X G V A G T A F
12	505.0 (+2)	T G A P V S E E G Y
12	513.7 (+2)	V Q X Y Y G S V V
12	519.0 (+2)	E P A M V X Z C F
12	531.2 (+2)	G Q P G A P X G G Z Y
12	541.0 (+2)	G P P H N G X R A Y
12	542.2 (+2)	A A H W H V E A Y
12	553.7 (+2)	T P P T R R E S Y
12	577.2 (+2)	F P T D R R S Q F
13	363.0 (+3)	Y T G V S Y X H F
13	447.0 (+2)	A Q A S A P D A Y
13	465.0 (+2)	V Q Y Y X P F
13	503.6 (+2)	G Q R K G A G S V F
13	553.2 (+2)	X Q Z X - - D V Y
13	590.8 (+2)	A T G T A Z N X N Z Y
14	460.7 (+2)	V V A P I T T G Y
14	471.5 (+2)	V V A C V - - - Y
14	495.2 (+2)	X Q Y T V G Y F
14	525.3 (+2)	P L A - N - H T Y
14	541.3 (+2)	P L F G Q T A G Q Y
14	550.4 (+2)	A - - - - Q X E Y
14	577.2 (+2)	Z G Y G N P X N G A Y
15	459.8 (+2)	V Q G P V G T D F
15	470.9 (+2)	V A G G W - - - F
15	514.2 (+2)	F Q A R X T E Y
15	536.6 (+2)	X A G F F X X E Y
15	544.2 (+2)	X Q - - - - Z Y
15	564.2 (+2)	S G A X D R A Y Z F
16	467.1 (+2)	F Q - - - - T X
16	500.4 (+2)	T P - - - A Z A F
16	501.0 (+2)	V V A T Z N Z Z X
16	503.6 (+2)	Y M V T - - - F
16	517.4 (+2)	A L G S Z A X M P F
16	521.3 (+2)	A P A V - - - V G Y
16	522.0 (+2)	V G Y V D D T Q F
16	525.6 (+2)	- - - - - T G F

TABLE A
CONT'D.

16	536.0 (+2)	P V P N V R X N Y
16	544.4 (+2)	- - - - - T X S X
16	557.6 (+2)	T L E G W M S Z Y
16	561.5 (+2)	Y M V C N A E E Y
16	596.7 (+2)	- - - - - X R D X Y
16	596.9 (+2)	S L X - - - - F
17	343.2 (+3)	A Q H P S <u>A</u> X R F
17	351.3 (+3)	A A F C G - - - X V
17	408.7 (+2)	Y L H - - E T
17	441.2 (+2)	- - - - - Z A Y
17	451.4 (+2)	I L G P P G S V Y
17	455.0 (+2)	G L G Z T S A E F
17	462.4 (+2)	X L G D V N M Y
17	483.8 (+2)	V M <u>G</u> <u>X</u> T N A N F
17	490.2 (+2)	N A X G R E S S F
17	497.2 (+2)	A M N P T N T V F
17	507.0 (+2)	- - - - X V E F
17	511.2 (+2)	X Q A P A X F V Y
17	519.2 (+2)	T A R V X S V E Y
17	526.8 (+2)	A L F - - - F T Y
17	542.8 (+2)	X Q X N A Y X S Y
17	563.2 (+2)	G L A R <u>C</u> <u>S</u> Z V E Y
18	503.8 (+2)	S Q X <u>A</u> <u>A</u> <u>G</u> V D V F
18	511.7 (+2)	P Q G Z M A - - Y
18	519.6 (+2)	- V F V S H T T F
18	538.8 (+2)	H X T G N E A T S F
18	565.7 (+2)	A E <u>F</u> <u>W</u> A C Z X Y
18	566.2 (+2)	Y M I D P S G V S Y
18	581.2 (+2)	X Q G H H E M F Y
20	448.2 (+2)	A A G X G P T F Y
20	560.0 (+2)	X V E X T T D Y Y
20	614.0 (+2)	I A V G Y V D D T Q F
21	507.2 (+2)	V A <u>F</u> <u>V</u> <u>X</u> F V G Y
22	510.8 (+2)	<u>A</u> L M P - - X N Y
22	557.2 (+2)	Y N <u>R</u> <u>W</u> S X E F
24	546.3 (+2)	- - Z D R N V T F
25	546.3 (+2)	V V T M - - - Z Y

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.

TABLE B

fraction	ion for MS/MS	derived peptide sequence
6	471.8 (+2)	A Z V E C E T Y
7	418.7 (+2)	A Q F A S G A G Z
7	504.2 (+2)	Z G X G G G P A T S Y
8	402.2 (+2)	- G - - C D Y
8	441.2 (+2)	- - - - - Z S F
8	516.9 (+2)	N Q Z H G S A E Y
9	331.4 (+3)	A P M A R G Z Y
9	349.4 (+3)	- - - - - G F Y
9	418.7 (+2)	A Z V N S G - Y
9	426.2 (+3)	A A S S Z V - - P P Z Y
9	433.3 (+2)	N P P A Z Z P N
9	437.0 (+2)	A C G G C G Z D Y
9	441.2 (+3)	- Z - D P P P D M Z Y
9	446.6 (+2)	G Q Z Z A V D F
9	578.0 (+2)	T P X G E P Y Z S Y
10	426.5 (+2)	G P - - - P Z Y
10	443.2 (+2)	A P Z Y P P P P
10	448.3 (+2)	G Z V C T P G S F
10	456.8 (+2)	C P L S C F T
10	464.7 (+2)	S Q F G G G S Q Y
10	465.4 (+2)	A S G F N G S Z Y
10	503.8 (+2)	- Z - - Y T A Y
10	508.7 (+2)	G Z P P H N G F Y
10	517.0 (+2)	I K A D H V S T Y
10	527.7 (+2)	X Z A D H V X P Y
10	540.2 (+2)	- - - - P G Z V Y
10	549.2 (+2)	Z S V - - - Z T G Y
11	437.0 (+2)	H X G N Q A A Y
11	511.4 (+2)	Z A G T T V P V S Y
11	527.4 (+2)	G Q Y P T Q P T Y
11	581.4 (+2)	F A G S Z S N T S T Y
12	494.8 (+2)	S Z G G - - - T G Y
12	526.8 (+2)	Z G P P N Y X T Y
12	547.1 (+2)	V K V I Q Q E S Y
13	454.6 (+2)	L P P P P P P P
13	476.0 (+2)	A K Y S T P A T L
13	503.6 (+2)	G Q R K G A G S V F
13	513.1 (+2)	R Z S A N H E A X
13	526.4 (+2)	G K V R T D I T Y
13	553.2 (+2)	V V X P A V R S T Y

TABLE B
CONT'D.

13	561.0 (+2)	A K Y P H V E D Y
13	571.3 (+2)	A Z N X S A Y V X Y
13	601.2 (+2)	E V V G D T Z Y
14	438.2 (+2)	A K A G I T T T L
14	490.8 (+2)	V - - T Z A G S A F
14	517.2 (+2)	A Z A A A N V X X Y
14	531.5 (+2)	A N H S V R D T Y
14	535.3 (+2)	E - - - G X R Z Y
14	552.8 (+2)	X Z H N D Z S T Y
14	577.2 (+2)	A N E Z X G - - - Y
15	497.3 (+2)	A A G P T A Z E S Y
15	514.2 (+2)	V A G X V F M Z Y
15	527.0 (+2)	A Z Y Z A Z V V F
15	564.2 (+2)	A Z F - - - Z X Y
15	577.2 (+2)	Z G Y G N P X N Z Y
15	626.0 (+2)	- - - - - Z A P C H Y
16	521.6 (+2)	A H A V Q R V V Y
16	525.6 (+2)	T Z X T V V X N Y
17	446.8 (+2)	A Z Z A S G X A F
17	492.8 (+2)	G S H S M R Y F
17	503.8 (+2)	Y G Y G A T V E F
17	967.6 (+1)	V Z - - - T T F
18	451.4 (+2)	Q P G P Q I V Y
18	455.2 (+2)	N G Z X S N N Y
18	475.2 (+2)	A N X V Z X E Y
18	489.1 (+2)	G Z - - - Z G X X Y
18	497.8 (+2)	A M N P T N T V F
18	525.2 (+2)	Y N - - - Z X F
18	538.8 (+2)	- M - - S Y Z N F
18	565.7 (+2)	A E <u>F</u> <u>W</u> A C Z X Y
19	521.6 (+2)	S Z F G <u>C</u> <u>P</u> T R F
19	524.6 (+2)	X G A X S N - - E F
19	571.2 (+2)	R Z A A Y R X T Y
19	646.2 (+2)	T N X H D G D G A T Z Y

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.

TABLE C

fraction	ion for MS/MS	derived peptide sequence
6	398.2 (+3)	- - W D R H T X F
6	448.2 (+2)	- - - - - Y T
8	419.2 (+2)	G S H F G V A Y
8	441.2 (+2)	V P <u>C</u> <u>G</u> <u>Z</u> <u>Z</u> S Y
8	473.2 (+2)	T A Z X H R G Y
8	512.8 (+2)	X A Z Y E H T Y
8	516.9 (+2)	N Q Z H G S A E Y
8	546.8 (+2)	N G <u>X</u> <u>A</u> <u>M</u> <u>H</u> W T Y
9	418.7 (+2)	F V S N H A Y
9	437.0 (+2)	T G - - - - A Y
9	465.2 (+2)	S Q F G G G S Q Y
9	476.2 (+2)	S Q F D H V T Y
9	481.0 (+2)	- P - - G Z D E V
9	514.2 (+2)	N G Y D G P N A G Y
9	578.0 (+2)	T P X G E P Y Z S Y
10	398.3 (+2)	X A N - - V T
10	448.3 (+2)	M P H S G Y G F
10	450.4 (+2)	V D X - - - Y
10	456.8 (+2)	C P L S C F T
10	464.7 (+2)	- - - - - P G F Y
10	486.2 (+2)	- A - P H P M G Y
10	494.2 (+2)	A Q T V G Y G E Y
10	508.7 (+2)	- - - - - S V Y
10	509.0 (+2)	F L Z A M Z S T Y
10	532.0 (+2)	T V X D S Z T H Y
11	444.1 (+2)	T P - - A R A P T
11	469.2 (+2)	S E H D R M Y
11	480.6 (+2)	T G N C S G T G T Y
11	496.8 (+2)	A Q V N P S X T Y
11	532.3 (+2)	S P G A E T R A X Y
12	473.2 (+2)	Y L G - - - G A F
12	494.8 (+2)	X T S F M Z V Y
12	499.0 (+2)	- P - - - P S S G Y
12	505.0 (+2)	T P - - - G R M Y
12	513.7 (+2)	P M F D Z Z V Y
12	519.0 (+2)	Y L - - - R T F
12	531.2 (+2)	A Q E H G C A A Z F
12	542.2 (+2)	- <u>M</u> - - - <u>G</u> <u>V</u> H D Y
12	550.2 (+2)	Y V S - - R N Q Y
12	553.7 (+2)	A Q Y A A G E S F Y

TABLE C
CONT'D.

12	564.0 (+2)	T P H T Z H D E Y
12	565.2 (+2)	Y M - - - F M Y
13	396.1 (+3)	D P H Y V S G H Z F
13	401.2 (+2)	M V G X X P A T
13	526.4 (+2)	Z A S P G E X T S Y
14	460.7 (+2)	V V A P I T T G Y
14	471.5 (+2)	V V A C V - - - Y
14	525.3 (+2)	P L A - N - H T Y
14	543.2 (+2)	X A X Y R R M Y
14	550.4 (+2)	P L A M Z X Y T Y
15	460.6 (+2)	- P - M P G X A Y
15	461.0 (+2)	H T T S Z N A Y
15	506.0 (+2)	M A A M V G V A V Y
15	508.4 (+2)	G P Z V M Z H G Y
15	514.2 (+2)	F Q A R X T E Y
15	520.0 (+2)	L P H Q P L A T Y
15	525.2 (+2)	A A A X V - - - V T Y
15	536.6 (+2)	X P E M G Z F S Y
15	544.2 (+2)	Y V - - V R - V F
15	564.2 (+2)	F V T X N X E E Y
16	489.0 (+2)	A A P V G A X E S Y
16	500.4 (+2)	G S - - - S Y T Y
16	522.0 (+2)	V G Y V D D T Q F
16	525.7 (+2)	Y V A - - - P A F
16	533.0 (+2)	V G Y - - A H P G F
16	535.7 (+2)	Z A T N S V T S T Y
16	537.0 (+2)	- - - - - S T Y
16	545.8 (+2)	Y A T A G E M M A F
16	547.0 (+2)	S P T Y T H A V A F
16	557.0 (+2)	M P A - - M V M A F
17	351.3 (+3)	A A F C G - - - X V
17	393.7 (+2)	S P N E D X M Z V F
17	403.2 (+2)	V A A T A G A V F
17	408.7 (+2)	Y L H - - E T
17	414.8 (+2)	T A F P F V F
17	451.4 (+2)	I L G P P G S V Y
17	462.4 (+2)	X L G D V N M Y
17	476.2 (+2)	Y G - - - V X S M
17	490.8 (+2)	X P H C S C S S F
17	504.0 (+2)	D P P C W G V S F
17	507.0 (+2)	- - - - X V E F
17	511.2 (+2)	- - - - A H D A Y
17	519.2 (+2)	T A R V X S V E Y
17	526.8 (+2)	X S D G R Z X T Y
17	542.8 (+2)	N M N D L V S E Y
17	557.2 (+2)	M P A A D Y E V A F
18	474.8 (+2)	A E I L Q V I Y
18	503.8 (+2)	A P - - - X V S Y

TABLE C CONT'D.

18	514.7 (+2)	M P A G Y N N V Y
18	519.6 (+2)	Y M S G <u>X</u> <u>Y</u> G T F
18	526.8 (+2)	- - - <u>A</u> <u>V</u> V A Z S Y
18	538.8 (+2)	X P V V P A A Z T Y
18	566.2 (+2)	Y M I D P S G V S Y
18	616.3 (+2)	F A N G V <u>Z</u> <u>G</u> <u>C</u> <u>A</u> <u>F</u> A F

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.

TABLE D

fraction	ion for MS/MS	derived peptide sequence
6	493.0 (+2)	N H A V G - - V S M
6	557.8 (+2)	H N V F Z P T S N A
7	434.8 (+2)	S V C E T E S X
7	481.3 (+2)	T H P S Z A C A F
7	489.1 (+2)	- H - - S P X X
8	420.1 (+2)	A N X E G P H T
8	441.7 (+2)	G H S P P T S S L
8	494.8 (+2)	C H S A F A L
8	511.6 (+2)	H H A F A Z V X V
8	519.4 (+2)	D H Y Y X A G S X
9	411.4 (+2)	E X A P H A A X
9	424.3 (+2)	A A A X R C E X
9	426.1 (+2)	G H Z A P A A S X
9	441.7 (+2)	V H N P Z S S X
9	444.2 (+2)	A G G P T X C R X
9	455.5 (+2)	L H L L T L E A
9	490.3 (+2)	A G G Z P A T P P A X
9	513.1 (+2)	S H Z G C V Z P A V
9	520.0 (+2)	X H R L C S P T X
10	404.2 (+2)	S V S X P H A P
10	417.1 (+2)	A P F T G G N G X
10	433.8 (+2)	G H D P D S P A A
10	446.2 (+2)	E H G X E N G H
10	455.4 (+2)	E H V A S S P A L
10	460.4 (+2)	H H A P C G V S X
10	464.0 (+2)	N H A I V S T S V
10	464.7 (+2)	G H Z N S V T S V
10	465.3 (+2)	S H Z A P C T S V
10	469.4 (+2)	F V A R F V S X
10	469.6 (+2)	H H S D G S V S L
10	473.7 (+2)	S H A G A P P P T X
10	482.6 (+2)	M C Z - G M P A X
10	482.8 (+2)	G H G A N N D P A X
10	495.7 (+2)	X H S Z P A G P A X
10	508.3 (+2)	X H V V S - - V X
10	511.2 (+2)	A V X D C C Z V A V
10	522.3 (+2)	E X G G N T N P Z X
10	522.7 (+2)	Y H G S Z N P E X
10	569.6 (+2)	- - - - - T Y S Y
10	574.3 (+2)	- - - - - - - M

TABLE D
CONT'D.

11	405.7 (+2)	S H - - - Y F
11	425.8 (+2)	A H P D Z A X V
11	444.7 (+2)	G T A H Y Z V X
11	448.9 (+2)	M H A D N P V X
11	455.7 (+2)	S H <u>V</u> <u>D</u> <u>R</u> P S X
11	459.7 (+2)	T G A A F Z N P X
11	482.8 (+2)	G H <u>C</u> <u>P</u> R N P A X
11	495.7 (+2)	X H S G A P Z A P X
11	516.7 (+2)	X H D <u>T</u> <u>E</u> <u>H</u> <u>A</u> P X
11	562.3 (+2)	- - - Y Z A Y V Y
12	411.7 (+2)	G H G P T X A A V
12	428.8 (+2)	V P - - - - -
12	444.7 (+2)	Y Q H T G A V L
12	448.4 (+2)	T Q A P G N P V L
12	460.3 (+2)	T Z A <u>G</u> <u>C</u> <u>M</u> <u>V</u> P X
12	490.9 (+2)	T H T Q P G V Q L
12	507.4 (+2)	G H A G H V P P E X
12	511.6 (+2)	T H F R Y V S X
12	528.1 (+2)	E H R P D R V F
13	427.6 (+2)	S H A Q T V V L
13	449.2 (+2)	S H A N S A V V L
13	464.8 (+2)	M V - - H P V X
13	487.6 (+2)	Y H H G G V S A F
13	506.2 (+2)	- H - - G H T G Y X
14	420.1 (+2)	N H A N G L T L
14	438.7 (+2)	- - - - - P X X
14	456.7 (+2)	A H S V P S P A F
14	477.7 (+2)	M H T - - P A P V
14	482.8 (+2)	P G A A V V P S X
14	560.8 (+2)	G H A G M G C V F Z X
14	592.3 (+2)	M R - - - - G X E X
15	418.9 (+2)	S H G V P R A X
15	439.0 (+2)	E H H M P X X
15	454.3 (+2)	H H Z C A A G A X
15	492.1 (+2)	X V D <u>Z</u> A <u>E</u> P X V
15	510.1 (+2)	I H T P E N P V I
15	520.0 (+2)	M G X P V R H M V
15	524.2 (+2)	S H Y D W Z V X
15	532.9 (+2)	M P H S H P F V X
15	577.2 (+2)	Z C V R C Z N G V F
16	412.9 (+2)	S H A G A G X V X
16	418.3 (+2)	G H X E G P X X
16	424.3 (+2)	X H G G D H V X
16	448.6 (+2)	E Z A H S X V X
16	448.9 (+2)	Y H H D X V X
16	454.3 (+2)	M A G A W C R X
16	456.7 (+2)	S H <u>D</u> <u>G</u> <u>S</u> V P T X
16	464.2 (+2)	F H - - X X X

**TABLE D
CONT'D.**

16	469.9 (+2)	E H - - - T V X
16	472.3 (+2)	M A X - - - V V
16	499.0 (+2)	G H A <u>X</u> <u>T</u> D G X T X
16	504.1 (+2)	P V <u>S</u> <u>H</u> <u>X</u> V N E L
16	507.7 (+2)	X X Y <u>T</u> <u>P</u> <u>G</u> H T X
16	522.7 (+2)	- - - - - P V X
16	523.3 (+2)	M A H S - - P V F
16	529.9 (+2)	X H Y D R N Q X
16	536.2 (+2)	E A - - C Z V T T Y
16	547.9 (+2)	- - - - - A X S V
16	552.4 (+2)	X Z <u>A</u> <u>P</u> <u>T</u> S V F Z X
17	367.7 (+3)	<u>E</u> <u>T</u> <u>M</u> <u>P</u> A H P S T X
17	490.8 (+2)	M T X G Y G E P X
17	557.3 (+2)	A H G R K M S K S L
17	340.7 (+3)	- <u>H</u> - - H A Z V X
17	367.7 (+3)	- - - - R X S H X
17	419.8 (+2)	- - - H A V G X X
17	462.8 (+2)	M S S N E X X M
17	476.2 (+2)	G H - - - P C C
17	504.2 (+2)	X H V X A V N E X
17	523.2 (+2)	- H - - - - P V F
17	543.2 (+2)	X H E V Z P H X X
17	590.2 (+2)	A T E H <u>C</u> <u>F</u> <u>V</u> M E X
18	456.4 (+2)	A H S N L A S V L
18	463.3 (+2)	V X A P A N D X X
18	474.8 (+2)	M X <u>G</u> <u>X</u> S F P A X
18	491.2 (+2)	V H T C V N P V X
18	497.8 (+2)	S H Q R Q L L L
18	515.8 (+2)	E W <u>H</u> <u>X</u> P V S X
18	519.7 (+2)	<u>E</u> H <u>M</u> <u>D</u> X Z T F
18	543.4 (+2)	X H E <u>V</u> <u>Z</u> P H X X
18	596.8 (+2)	<u>E</u> <u>H</u> <u>H</u> <u>T</u> Z S N P X X
19	434.6 (+2)	- H <u>G</u> <u>C</u> <u>P</u> G M P X
19	496.6 (+2)	<u>E</u> <u>T</u> <u>P</u> <u>E</u> H A P V X
19	539.6 (+2)	<u>M</u> <u>X</u> P G N S A X Y X

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.

TABLE E

fraction	ion for MS/MS	derived peptide sequence
7	504.1 (+2)	H M S G Z P T S Y
7	549.2 (+2)	H N Z A A H Z E Y
8	517.0 (+2)	N Q Z H G S A E Y
8	526.0 (+2)	H A A <u>X</u> <u>Y</u> <u>S</u> Z V Y
8	642.7 (+2)	P M N D W X M T Z T Y
10	465.3 (+2)	S Q F G G G S Q Y
10	484.3 (+2)	Y Q S <u>D</u> <u>H</u> R Y
10	509.0 (+2)	F L Z A M Z S T Y
10	532.0 (+2)	T V X D S Z T H Y
11	424.3 (+2)	H X S T Z D F
11	464.3 (+2)	H A P P T D P P P
11	550.0 (+2)	H G P A N <u>R</u> <u>D</u> <u>S</u> V F
11	563.3 (+2)	F P Y P T D P Z Y
12	531.2 (+2)	K N A N L V Q L Y
14	585.6 (+2)	R S F X X E N E Y
16	488.7 (+2)	H M Z N P T S Y
16	661.9 (+2)	Y V X F - - - V Y
17	577.6 (+2)	R S M X <u>R</u> <u>C</u> <u>P</u> E Y
18	451.1 (+2)	I L G P P G S V Y
18	523.0 (+2)	- - <u>E</u> <u>V</u> <u>T</u> A Z T Y
19	565.6 (+2)	Y M I D P S G V S Y
19	503.8 (+2)	S Q X A A G V D V F
20	560.0 (+2)	X V E X T T D Y Y
20	582.4 (+2)	M Y N <u>C</u> <u>N</u> E X D Y
21	448.2 (+2)	A A G X G P T F Y
21	614.0 (+2)	I A V G Y V D D T Q F
22	507.2 (+2)	V A <u>E</u> <u>V</u> <u>X</u> F V G Y
22	557.2 (+2)	Y N <u>R</u> <u>W</u> S X E F
23	510.8 (+2)	<u>A</u> <u>L</u> M P - - X N Y
25	562.8 (+2)	N Q F Q A L L Q Y

* Dashes represent positions at which amino acids could not be unambiguously assigned through NanoES-MS/MS fragmentation patterns and/or Edman data obtained. Underlined residues designate tentative assignments.